```
1                                                  31
TCG ACT ATG AAT GCA GAT ACA GCT CCA ACA TCT CCT TGT CCT TCC ATA TCT TCC CAG AAC
ser thr met asn ala asp thr ala pro thr ser pro cys pro ser ile ser ser gln asn

61                                                 91
TCA AGC TCC TGC TCC AGC TTC CAG GAC CAG AAG ATC GCC AGC ATG TTC GAT CGG ACT TCC
ser ser ser cys ser ser phe gln asp gln lys ile ala ser met phe asp arg thr ser

                                                        Cadherin
121                                               151       xx EC motif xx|
AGA GTA CCC GCC AGC AGC ACT TCC TCA CCG GGG CTC CTC TTC ACA GAA CTG GCT GCT GCC
arg val pro ala ser ser thr ser ser pro gly leu leu phe thr glu leu ala ala ala

181                                               211
CTG GAT GCC GAA GGG GAA GGA ATC AGC GAA GTA CAA AGG AAA GCT GTC AGT GCA ATT CAC
leu asp ala glu gly glu gly ile ser glu val gln arg lys ala val ser ala ile his

241                                               271
AGC CTG CTA AGT TCT GAC GAC CTG GAC CCA CGC TGT GTC AAA CCA GAG GTG AAG GTC AAA
ser leu leu ser ser his asp leu asp pro arg cys val lys pro glu val lys val lys

301                                               331
ATC GCC GCC CTT TAC CTA CCT TTA GTT GGC ATC ATT TTG GAT GCT TTG CCA CAG CTC TGT
ile ala ala leu tyr leu pro leu val gly ile ile leu asp ala leu pro gln leu cys

361                                               391
GAC TTT ACA GTT GCA GAT ACT CGC AGA TAC CGC ACC AGT GGC TCG GAT GAA GAA CAA GAA
asp phe thr val ala asp thr arg arg tyr arg thr ser gly ser asp glu glu gln glu

421                                               451
GGA GCC AGT GCC ATT ACC CAG AAT GTG GCT CTG GCC ATA GCA GGG AAT AAT TTC AAT TTG
gly ala gly ala ile thr gln asn val ala leu ala ile ala gly asn asn phe asn leu

481                                               511
AAA ACA AGT GGA ATA GTG CTG TCT TCC TTG CCC TAT AAG CAG TAC AAC ATG CTG AAC GCG
lys thr ser gly ile val leu ser ser leu pro tyr lys gln tyr asn met leu asn ala

541                                               571
GAC ACT ACT CGC AAC CTC ATG ATC TGC TTC CTC TGG ATC ATG AAA AAT GCT GAT CAG AGC
asp thr thr arg asn leu met ile cys phe leu trp ile met lys asn ala asp gln ser

601                                               631
CTC ATT AGG AAG TGG ATT GCT GAC CTG CCA TCA ACG CAG CTC AAC AGG ATT TTA GAT CTA
leu ile arg lys trp ile ala asp leu pro ser thr gln leu asn arg ile leu asp leu

661                                               691
TTT TGT ATT TCT TTG TTA TTT TTA GAT GAT AAT TGA AAA TAT AGT TTT GAT AAA GTT AGT
leu phe ile tyr val leu tyr phe glu tyr lys gly lys glu met met asp lys val ser

721                                               751
ACC CAA GTC CTG CAG AAG TCA AGG GAT GTC AAG GCC CGG CTG GAA GAG GCT TTG CTG CGT
thr gln val leu gln lys ser arg asp val lys ala arg leu glu glu ala leu leu arg

781                                               811
GGG GAA GGG GCT AGA TGG GAG ATG ATG CTC TGC CGG TTT CTA GGG AAC GAC CGA TTT CTA
```

FIG. 1 (1 of 5)

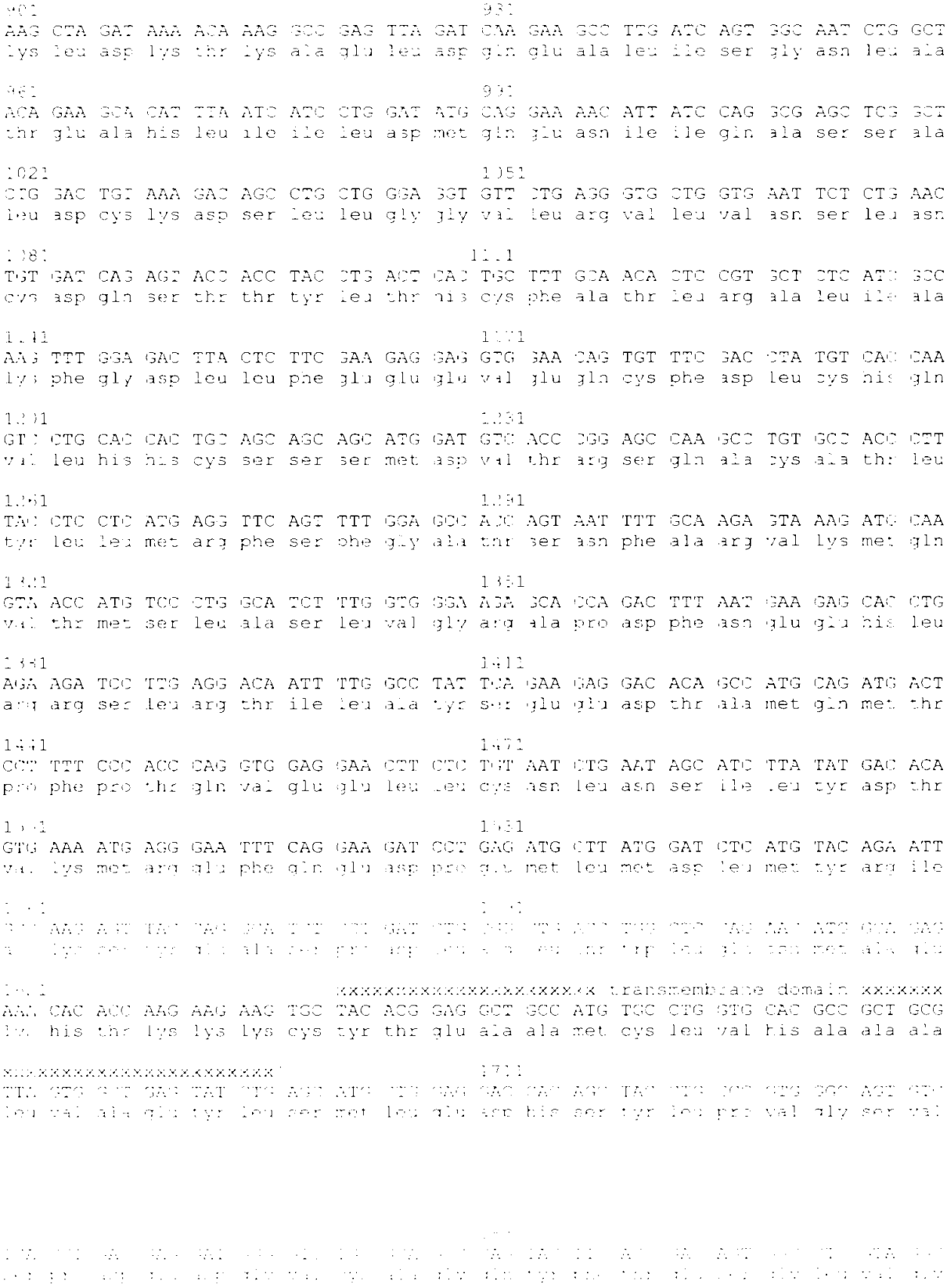

AAG CTA GAT AAA ACA AAG GCC GAG TTA GAT CAA GAA GCC TTG ATC AGT GGC AAT CTG GCT
lys leu asp lys thr lys ala glu leu asp gln glu ala leu ile ser gly asn leu ala
ACA GAA GCA CAT TTA ATC ATC CTG GAT ATG CAG GAA AAC ATT ATC CAG GCG AGC TCG GCT
thr glu ala his leu ile ile leu asp met gln glu asn ile ile gln ala ser ser ala
CTG GAC TGT AAA GAC AGC CTG CTG GGA GGT GTT CTG AGG GTG CTG GTG AAT TCT CTG AAC
leu asp cys lys asp ser leu leu gly gly val leu arg val leu val asn ser leu asn
TGT GAT CAG AGT ACC ACC TAC CTG ACT CAT TGC TTT GCA ACA CTC CGT GCT CTC ATT GCC
cys asp gln ser thr thr tyr leu thr his cys phe ala thr leu arg ala leu ile ala
AAG TTT GGA GAC TTA CTC TTC GAA GAG GAG GTG GAA CAG TGT TTC GAC CTA TGT CAC CAA
lys phe gly asp leu leu phe glu glu glu val glu gln cys phe asp leu cys his gln
GTC CTG CAC CAC TGC AGC AGC AGC ATG GAT GTC ACC CGG AGC CAA GCC TGT GCC ACC CTT
val leu his his cys ser ser ser met asp val thr arg ser gln ala cys ala thr leu
TAC CTC CTC ATG AGG TTC AGT TTT GGA GCC ACC AGT AAT TTT GCA AGA GTA AAG ATG CAA
tyr leu leu met arg phe ser phe gly ala thr ser asn phe ala arg val lys met gln
GTA ACC ATG TCC CTG GCA TCT TTG GTG GGA AGA GCA CCA GAC TTT AAT GAA GAG CAC CTG
val thr met ser leu ala ser leu val gly arg ala pro asp phe asn glu glu his leu
AGA AGA TCC TTG AGG ACA ATT TTG GCC TAT TCA GAA GAG GAC ACA GCC ATG CAG ATG ACT
arg arg ser leu arg thr ile leu ala tyr ser glu glu asp thr ala met gln met thr
CCT TTT CCC ACC CAG GTG GAG GAA CTT CTC TGT AAT CTG AAT AGC ATC TTA TAT GAC ACA
pro phe pro thr gln val glu glu leu leu cys asn leu asn ser ile leu tyr asp thr
GTG AAA ATG AGG GAA TTT CAG GAA GAT CCT GAG ATG CTT ATG GAT CTC ATG TAC AGA ATT
val lys met arg glu phe gln glu asp pro glu met leu met asp leu met tyr arg ile
AAC CAC ACC AAG AAG AAG TGC TAC ACG GAG GCT GCC ATG TGC CTG GTG CAC GCC GCT GCG
lys his thr lys lys lys cys tyr thr glu ala ala met cys leu val his ala ala ala
TTA GTG GAT GAA TAT CTG AGT ATG TTT GAG GAC AAA AGT TAT CTG GCT CTG GCC AGT GTT
leu val ala glu tyr leu ser met leu glu asp his ser tyr leu pro val gly ser val

FIG. 1 (2 of 5)

1861 1891
CTC CTG GAG CAG GCC GCG GAG CTC TTC AGC ACG GGA GGC TTA TAT GAG ACA GTT AAT GAG
leu leu glu gln ala ala glu leu phe ser thr gly gly leu tyr glu thr val asn glu

1921 1951
GTC TAC AAG CTG GTC ATC CCC ATC CTA GAA GCG CAT CGA GAA TTC CGG AAG CTG ACA CTC
val tyr lys leu val ile pro ile leu glu ala his arg glu phe arg lys leu thr leu

1981 2011
ACT CAC AGC AAG CTG CAG AGA GCC TTC GAC AGC ATC GTT AAC AAG GAT CAT AAG AGA ATG
thr his ser lys leu gln arg ala phe asp ser ile val asn lys asp his lys arg met

2041 |xxxxx ITAM xxxx| 2071
TTT GGA ACC TAC TTC CGA GTT GGT TTC TTT GGA TCC AAA TTT GGG GAT TTG GAT GAA CAG
phe gly thr tyr phe arg val gly phe phe gly ser lys phe gly asp leu asp glu gln

2101 2131
GAG TTT GTC TAC AAA GAG CCT GCA ATT ACC AAG CTT CCT GAG ATC TCA CAT AGA CTA GAG
glu phe val tyr lys glu pro ala ile thr lys leu pro glu ile ser his arg leu glu

2161 2191
GCA TTT TAT GGT CAA TGT TTT GGT GCA GAA TTT GTG GAA GTG ATT AAA GAC TCC ACT CCT
ala phe tyr gly gln cys phe gly ala glu phe val glu val ile lys asp ser thr pro

2221 2251
GTG GAC AAA ACC AAG TTG GAT CCT AAC AAG GCC TAC ATA CAG ATC ACT TTT GTG GAG CCC
val asp lys thr lys leu asp pro asn lys ala tyr ile gln ile thr phe val glu pro

2281 2311
TAC TTT GAT GAG TAT GAG ATG AAA GAC AGG GTC ACA TAC TTT GAG AAG AAT TTC AAC CTC
tyr phe asp glu tyr glu met lys asp arg val thr tyr phe glu lys asn phe asn leu

2341 2371
CGG AGG TTC ATG TAC ACC ACC CCG TTC ACC CTG GAG GGG CGG CCT CGG GGA GAG CTG CAT
arg arg phe met tyr thr thr pro phe thr leu glu gly arg pro arg gly glu leu his

2401 2431
GAG CAG TAC AGA AGG AAC ACA GTC CTG ACC ACT ATG CAC GCC TTC CCC TAC ATC AAG ACC
glu gln tyr arg arg asn thr val leu thr thr met his ala phe pro tyr ile lys thr

2461 2491 |xxxxxxxxxxxxxxxxxxxxxx
AGG ATC AGC GTC ATC CAG AAG GAG GAG TTT GTT TTG ACA CCG ATT GAA GTT GCC ATT GAA
arg ile ser val ile gln lys glu glu phe val leu thr pro ile glu val ala ile glu

2521 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx [illegible] xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
GAT ATG AAG AAG AAG ACT CTG CAT TTA GCA GTT GCC ATT AAT CAG GAG CCG CCT GAT GCA
asp met lys lys lys thr leu his leu ala val ala ile asn gln glu pro pro asp ala

2581 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx 2611
AAG ATG CTT CAG ATG GTG CTG CAA GGC TCT GTG GGA GCT ACT GTA AAT CAG GGA CCA CTG
lys met leu gln met val leu gln gly ser val gly ala thr val asn gln gly pro leu

2641 2671
GAA GTA GCC CAA GTG TTT TTG GCT GAA ATT CCT GCT GAT CCA AAA CTC TAT CGA CAT CAC
glu val ala gln val phe leu ala glu ile pro ala asp pro lys leu tyr arg his his

[illegible]
[illegible]
[illegible]

FIG. 1 (3 of 5)

```
xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx|
AAC AAG CTA AAA GAG AAC CTC AGG CCA ATG ATC GAG CGG AAA ATT CCA GAA CTG TAC AAG
asn lys leu lys glu asn leu arg pro met ile glu arg lys ile pro glu leu tyr lys

2881                                                2911
CCA ATA TTT AGA GTT GAG AGT CAA AAG AGG GAT TCT TTC CAC AGA TCT AGT TTC AGG AAA
pro ile phe arg val glu ser gln lys arg asp ser phe his arg ser ser phe arg lys

2941                                                2971
TGT GAA ACC CAG TTG TCA CAG GGC AGC TAA GAA AAG CCA TCT TCA TTC GTG GAG ACT GTG
cys glu thr gln leu ser gln gly ser OCH glu lys pro ser ser phe val glu thr val

3001                                                3031
GCC CTG CAA CCC TGG AGA AGG ACT TGC TGG TAC TTA AAA AAT GGG ACA TTT GCC ACC CAG
ala leu gln pro trp arg arg thr cys trp tyr leu lys asn gly thr phe ala thr gln

3061                                               3091
GAC TGA CTG TAC ACT CCC TGA TCA GCC AGC ACT CTG GAA GCT TTG GGA TCC CAG GAA CCA
asp STP

3121                                                3151
TGG AAT TAT TCC CAA ATG GAC TCT GAC CAG ACT TTT GCC ATA CTG GGG GGT GGC GGG ATG

3181                                                3211
GAG GAT GGG TAC TCA GGC ATG ACT GCG TAT TTA TTA AAG TGT GTT TTT CCA CAA TGT ACC

3241                                                3271
AAA CAA GGC ATA AGC AGC TTC TCC TGC TGA CTG GCC AAT CAC TGC CCA TCT GAG AGA TGA

3301                                                3331
TTT CCT CTG GCC CAT ATT TGA ATT TAT TGG AGT AAC TCA AAT TGC CTG AGG AAA AAT GGA

3361                                                3391
AAA ATT ATC CAC CAG TCG ATT CAA ACT GAA TTT CAC TCT TTA TAG GAA GGC AGG GCA AAC

3421                                                3451
TTG TAG GAG TAC GAA ACA TTT TCA ATA AAT CTA CAA AGG GAA GCC TTA CTA CAA TTC CAA

3481                                                3511
AAA TCA TCA TGC TTG GAA ATT TGG GAG GAG ATT ATT TGT GAA CTT GTT ACC CTT TTG GTA

3541                                                3571
ATG GTG GAT TAA TTT CTG TAT AGT TAT TTT TGT TTT ATT ATT ACT GTT ACA TTA ATT TAA

 ...                                                ...
TAT TTA TTT ATA TAA GAA TAT ATT CAA ATT AAT GAT CTA TGA GAT ATA TGT TAT TTC GAG

...                                                ...
CAG TCA GCC AAA AAT CAC AGA TAC TGC TTT CAC TTA AAT GGA AAC AAT TCT CCG ATA ATG

3721                                               3751
CTT TGC TTT TTT TCT TAT GTC ACT CTT GTG TAC TAT CTA TTT TTC TCC TCT CTG GGA CCA

...                                                ...
AGT TTT TTT TTA TAA AAT AAT ATT TAT TTT TTT ATT TTA GAA CAT TGT GTT GTC TGT
```

FIG. 1 (4 of 5)

4021
AAC TCG

FIG. 1 (5 of 5)

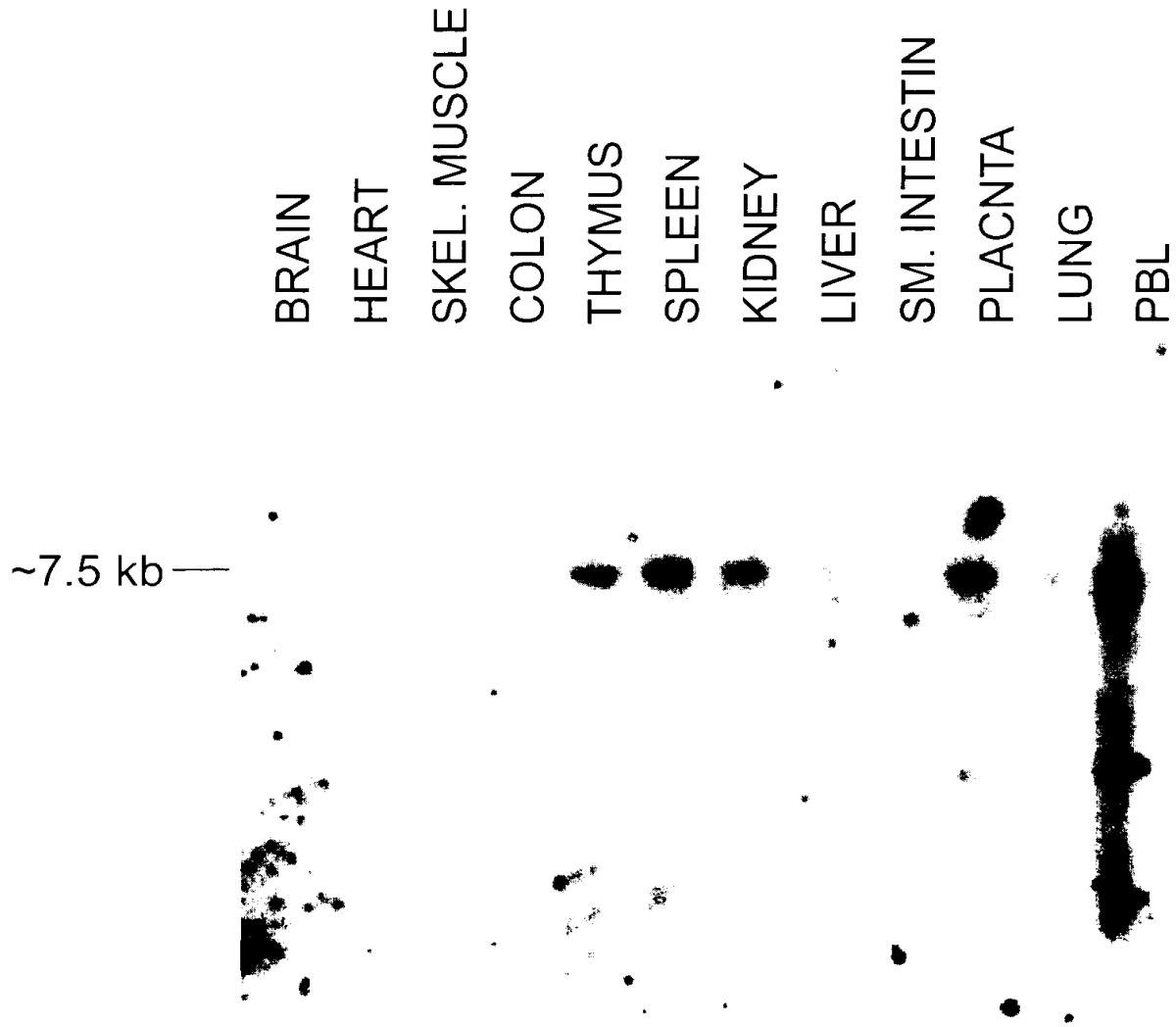

BRAIN
HEART
SKEL. MUSCLE
COLON
THYMUS
SPLEEN
KIDNEY
LIVER
SM. INTESTIN
PLACNTA
LUNG
PBL
~7.5 kb

FIG. 2A

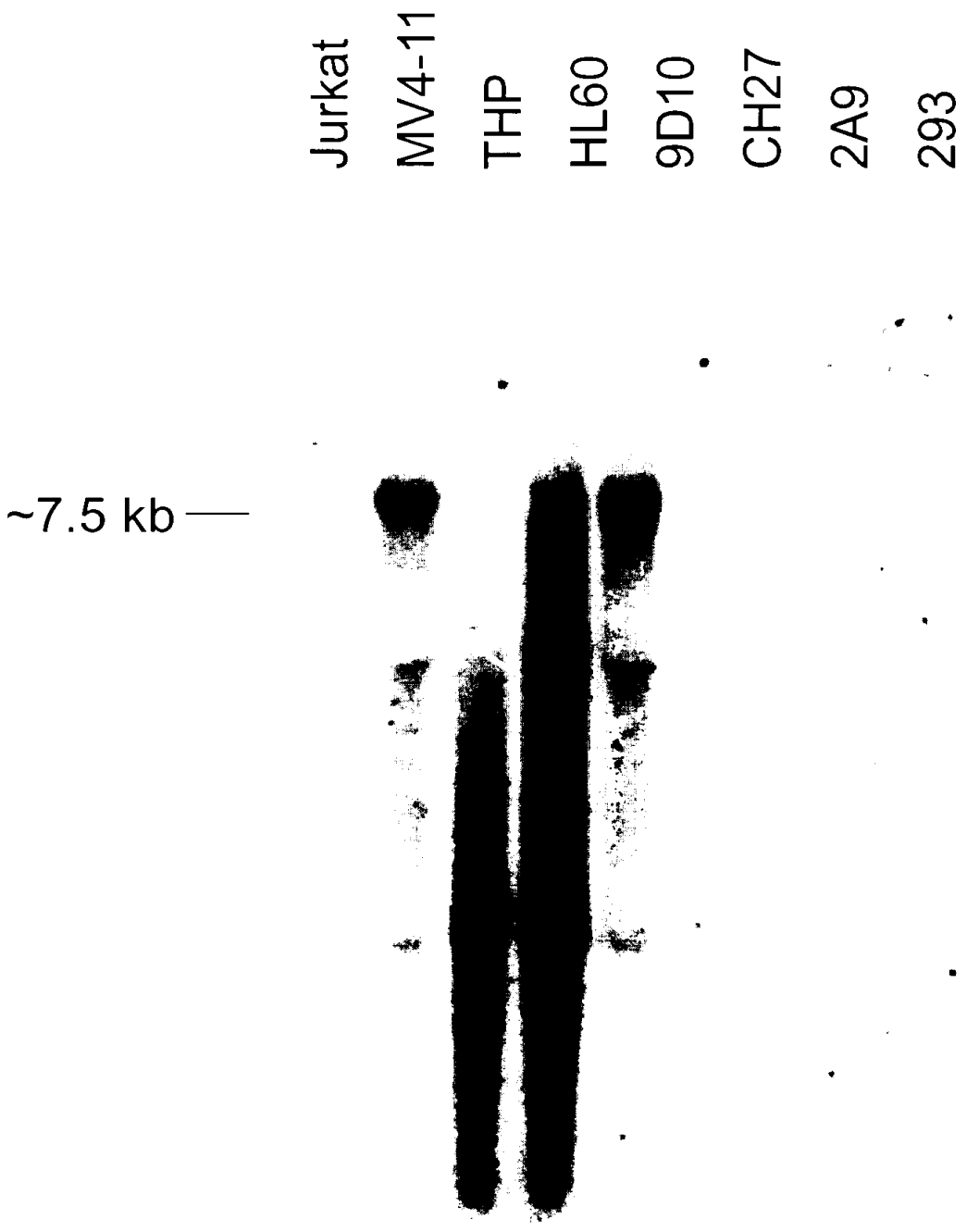


FIG. 2B

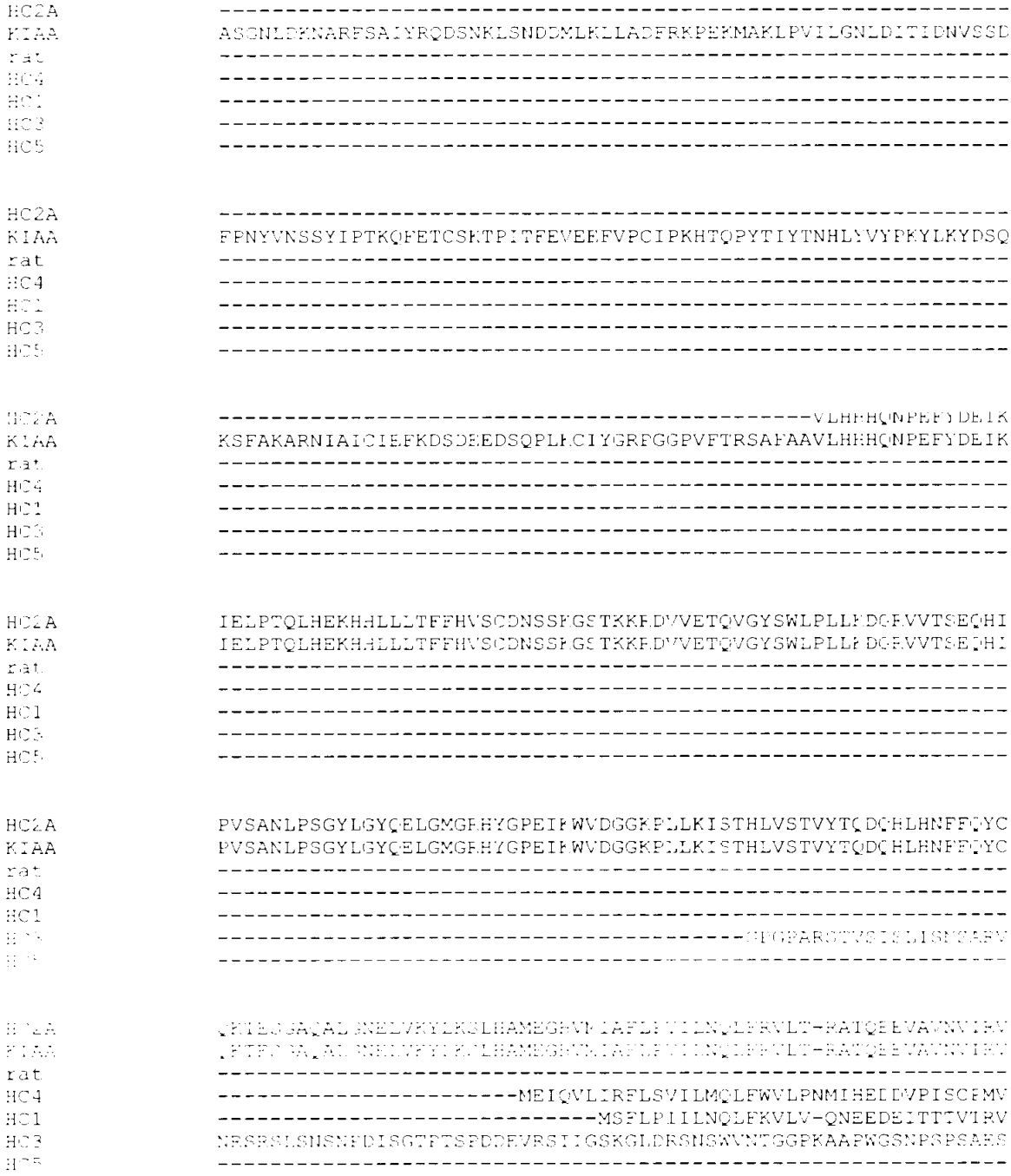


FIG. 3A (1 of 5)

FIG. 3A (2 of 5)

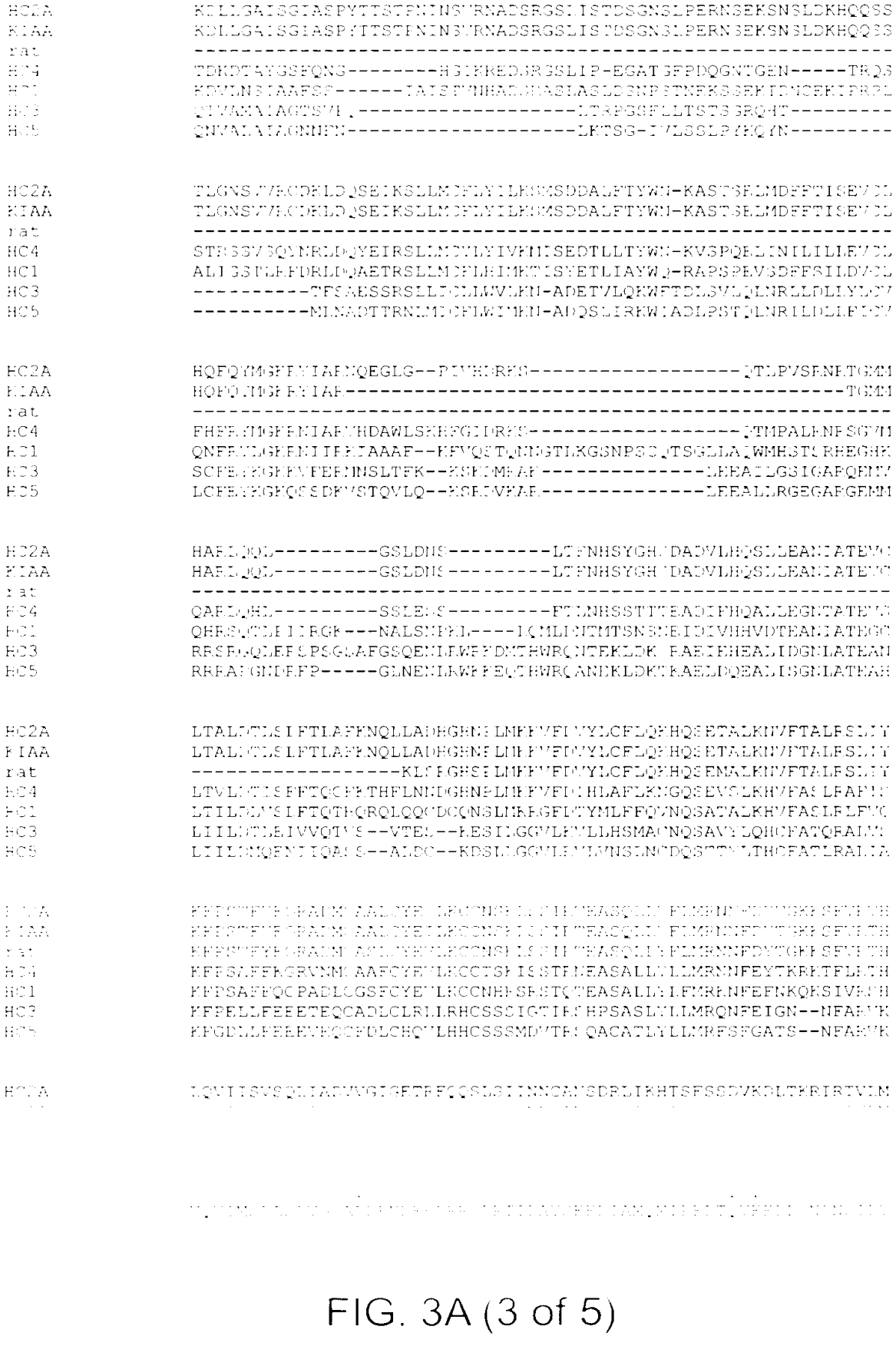


FIG. 3A (3 of 5)

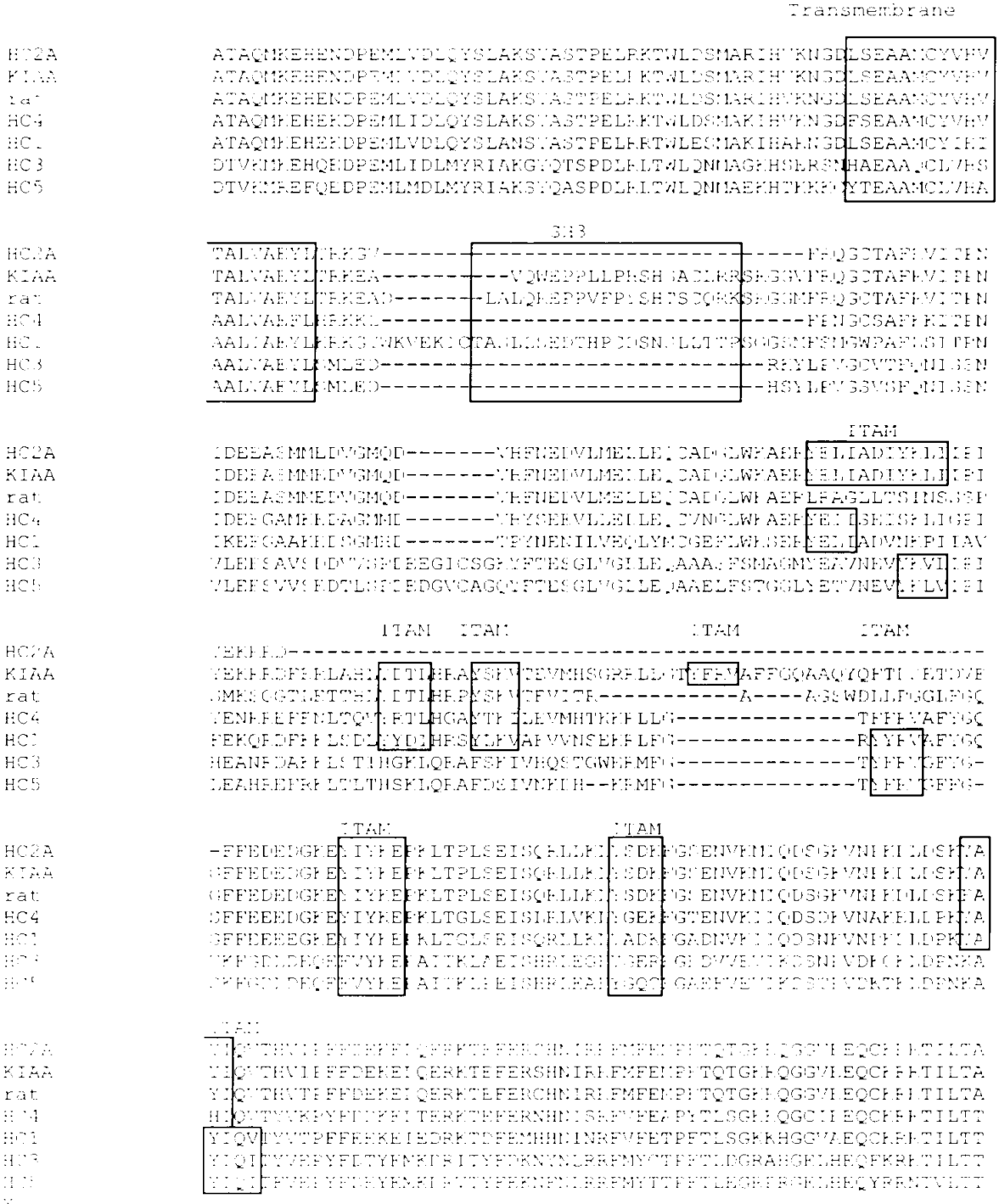

Transmembrane
HC2A
KIAA
rat
HC4
HC1
HC3
HC5
SH3
ITAM
ITAM
ITAM
ITAM
ITAM
ITAM
ITAM

FIG. 3A (4 of 5)


Coiled-Coil 1
Coiled-Coil 2
Coiled-Coil 2
PEM
HC2A
KIAA
rat
HC4
HC1
HC3
HC5

FIG. 3A (5 of 5)

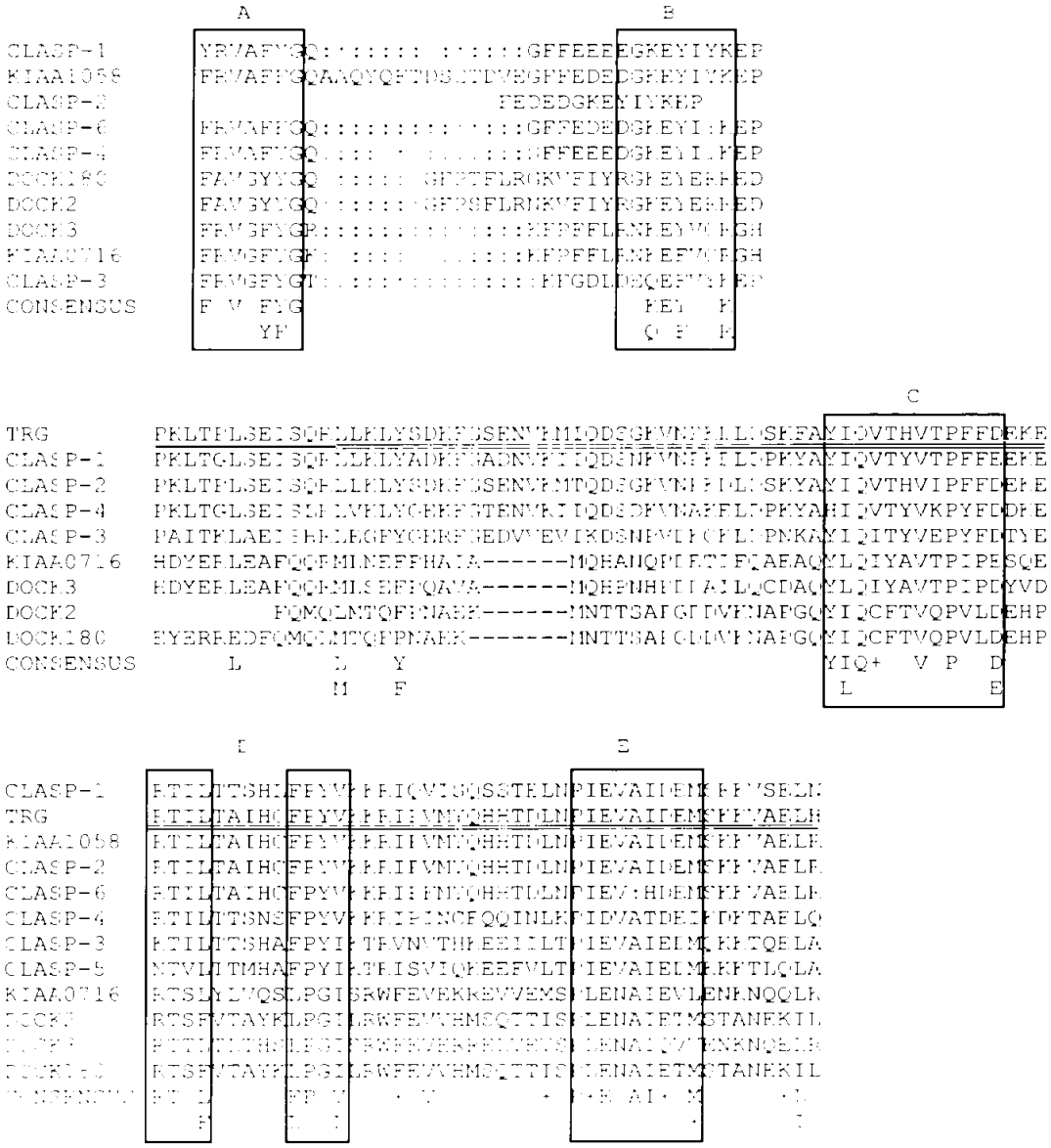
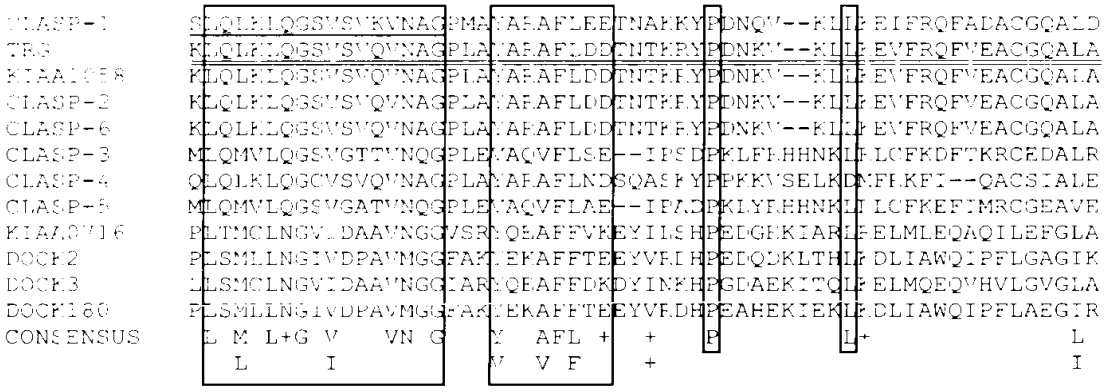

A
B
C
D
E
CLASP-1
KIAA1058
CLASP-2
CLASP-6
CLASP-4
DOCK180
DOCK2
DOCK3
KIAA0716
CLASP-3
CONSENSUS
TRG

FIG. 3B (1 of 2)



DOCK2=KIAA0209
DOCK3=KIAA0299
CLASP2variant=KIAA1058

FIG. 3B (2 of 2)

FIG. 4A (1 of 7)

```
                                                  871
CGT CTA AAT GAA AAT TTG AGA TGG AAG AAA GAG CAG ACA CAT TGG CGG CAA GCT AAT GAG
arg leu asn glu asn leu arg trp lys lys glu gln thr his trp arg gln ala asn gln

                                                  931
AAG CTA GAT AAA ACA AAG GCC GAG TTA GAT CAA GAA GCC TTG ATC AGT GGC AAT CTG GCT
lys leu asp lys thr lys ala glu leu asp gln glu ala leu ile ser gly asn leu ala

                                                  991
ACA GAA GCA CAT TTA ATC ATC CTG GAT ATG CAG GAA AAC ATT ATC CAG GCG AGC TCG GCT
thr glu ala his leu ile ile leu asp met gln glu asn ile ile gln ala ser ser ala

1021                                             1051
CTG GAC TGT AAA GAC AGC CTG CTG GGA GGT GTT CTG AGG GTG CTG GTG AAT TCT CTG AAC
leu asp cys lys asp ser leu leu gly gly val leu arg val leu val asn ser leu asn
                                                      ref 3.1
1081                                             1111
TGT GAT CAG AGT ACC ACC TAC CTG ACT CAC TGC TTT GCA ACA CTC CGT GCT CTC ATC GCC
cys asp gln ser thr thr tyr leu thr his cys phe ala thr leu arg ala leu ile ala

1141                                             1171
AAG TTT GGA GAC TTA CTC TTC GAA GAG GAG GTG GAA CAG TGT TTC GAC CTA TGT CAC CAA
lys phe gly asp leu leu phe glu glu glu val glu gln cys phe asp leu cys his gln

1201                                             1231
GTC CTG CAC CAC TGC AGC AGC AGC ATG GAT GTC ACC CGG AGC CAA GCC TGT GCC ACC CTT
val leu his his cys ser ser ser met asp val thr arg ser gln ala cys ala thr leu

1261                                             1291
TAC CTC CTC ATG AGG TTC AGT TTT GGA GCC ACC AGT AAT TTT GCA AGA GTA AAG ATG CAA
tyr leu leu met arg phe ser phe gly ala thr ser asn phe ala arg val lys met gln

1321                                             1351
GTA ACC ATG TCC CTG GCA TCT TTG GTG GGA AGA GCA CCA GAC TTT AAT GAA GAG CAC CTG
val thr met ser leu ala ser leu val gly arg ala pro asp phe asn glu glu his leu

1381                                             1411
AGA AGA TCC TTG AGG ACA ATT TTG GCC TAT TCA GAA GAG GAC ACA GCC ATG CAG ATG ACT
arg arg ser leu arg thr ile leu ala tyr ser glu glu asp thr ala met gln met thr

1441                                             1471
CCT TTT GCC AGC CAG GTG GAG GAA CTT CTC TGT AAT CTG AAT AGC ATC TTA TAT GAC ACA
pro phe ala ser gln val glu glu leu leu cys asn leu asn ser ile leu tyr asp thr

1501                                             1531
GTT AAA ATT AAA GAA TTT TAT GAA GAT CTT GAG ATT TTT ATG TAT GTT ATG TAT AGA ATT
val lys met arg glu phe tyr glu asp leu glu met leu met asp leu met tyr arg ile

1561                                             1591
GCT AAG AGT TAT CAG GCA TTT CCT GAT CTG CGG CTG ACC TGG CTC CAG AAC ATG GCA GAG
ala lys ser tyr gln ala ser pro asp leu arg leu thr trp leu gln asn met ala glu

1621                                             1651
AAA TAT ATT AAT AAA AAG TTT TAT ATT GAT GTT TTT ATT TTT TTT TAT GCT CTT TCT
lys tyr ile asn lys lys phe tyr ile asp val phe ile phe phe tyr ala leu ser
```

FIG. 4A (2 of 7)

1681 1711
TTA GTG GCT GAG TAT CTG AGC ATG CTG GAG GAC CAC AGC TAC CTG CCC GTG GGC AGT GTC
leu val ala glu tyr leu ser met leu glu asp his ser tyr leu pro val gly ser val

1741 1771
AGC TTC CAG AAT ATT TCT TCC AAT GTG CTG GAG GAG TCT GTG GTC TCT GAG GAC ACC CTG
ser phe gln asn ile ser ser asn val leu glu glu ser val val ser glu asp thr leu

1801 1831
TCA CCT GAC GAG GAT GGG GTG TGC GCA GGC CAG TAC TTC ACC GAG AGT GGC CTG GTA GGC
ser pro asp glu asp gly val cys ala gly gln tyr phe thr glu ser gly leu val gly

1861 1891
CTC CTG GAG CAG GCC GCG GAG CTC TTC AGC ACG GGA GGC TTA TAT GAG ACA GTT AAT GAG
leu leu glu gln ala ala glu leu phe ser thr gly gly leu tyr glu thr val asn glu

1921 1951
GTC TAC AAG CTG GTC ATC CCC ATC CTA GAA GCG CAT CGA GAA TTC CGG AAG CTG ACA CTC
val tyr lys leu val ile pro ile leu glu ala his arg glu phe arg lys leu thr leu

1981 2011
ACT CAC AGC AAG CTG CAG AGA GCC TTC GAC AGC ATC GTT AAC AAG GAT CAT AAG AGA ATG
thr his ser lys leu gln arg ala phe asp ser ile val asn lys asp his lys arg met

2041 2071
TTT GGA ACC TAC TTC CGA GTT GGT TTC TTT GGA TCC AAA TTT GGG GAT TTG GAT GAA CAG
phe gly thr tyr phe arg val gly phe phe gly ser lys phe gly asp leu asp glu gln

2101 2131
GAG TTT GTC TAC AAA GAG CCT GCA ATT ACC AAG CTT CCT GAG ATC TCA CAT AGA CTA GAG
glu phe val tyr lys glu pro ala ile thr lys leu pro glu ile ser his arg leu glu

2161 2191
GCA TTT TAT GGT CAA TGT TTT GGT GCA GAA TTT GTG GAA GTG ATT AAA GAC TCC ACT CCT
ala phe tyr gly gln cys phe gly ala glu phe val glu val ile lys asp ser thr pro

ref 4.1

2221 2251
GTG GAC AAA ACC AAG TTG GAT CCT AAC AAG GCC TAC ATA CAG ATC ACT TTT GTG GAG CCC
val asp lys thr lys leu asp pro asn lys ala tyr ile gln ile thr phe val glu pro

2281 2311
TAC TTT GAT GAG TAT GAG ATG AAA GAC AGG GTC ACA TAC TTT GAG AAG AAT TTC AAC CTC
tyr phe asp glu tyr glu met lys asp arg val thr tyr phe glu lys asn phe asn leu

2341 2371
[illegible] AGG TTT ATG TAT ACC ACC [illegible] TTC A[illegible] CTG GAG [illegible] [illegible] [illegible] [illegible] GGA GAG CTG CAT
arg arg phe met tyr thr thr pro phe thr leu glu gly arg pro arg gly glu leu his

2401 2431
GAG CAG TAC AGA AGG AAC ACA GTC CTG ACT ACT ATG CAC GCC TTC CCC TAC ATC AAG ACC
glu gln tyr arg arg asn thr val leu thr thr met his ala phe pro tyr ile lys thr

2461 2491
[illegible]
arg ile [illegible] val ile [illegible] lys [illegible] [illegible] phe val [illegible] thr pro ile glu val ala ile [illegible]

FIG. 4A (3 of 7)

```
2521                                                2581
GA ATG AAG AAG AAG ACT CTG CAG TTA GCA GTT GCC ATT AAC CAG GAG CCG CCT GAT GCA
asp met lys lys lys thr leu gln leu ala val ala ile asn gln glu pro pro asp ala

2641                                                2701
AAG ATA TTT TAT ATA GTG CTG AAA GGT TTT GTG GGA GTT ACT GTA AAT CAG GGA CCA CTG
lys met phe gln met val leu asp gly met val gly ala thr val asn gln gly pro leu

2761                                                2821
GAA GTA GCC CAA GTG ITT TTG GCT GAA ATT GCT GCT GAT CCA AAA CTC TAT CGA CAT CAC
glu val ala gln val phe leu ala glu ile pro ala asp pro lys leu tyr arg his his

2881                                                2941
AAC AAG TTG AGG TTA TGC TTT AAG GAA TTC ATC ATG AGA TGT GGT GAA GCT GTA GAG AAA
asn lys leu arg leu cys phe lys glu phe ile met arg cys gly glu ala val glu lys

3001                                                3061
AAC AAG CGT CTC ATC ACG GCA GAC CAG AGG GAA TAT CAG CAG GAA CTC AAA AAG AAC TAT
asn lys arg leu ile thr ala asp gln arg glu tyr gln gln glu leu lys lys asn tyr

2821                                                2881
AAC AAG CTA AAA GAG AAC CTC AGG CCA ATG ATC GAG CGG AAA ATT CCA GAA CTG TAC AAG
asn lys leu lys glu asn leu arg pro met ile glu arg lys ile pro glu leu tyr lys

2881                                                2941
CCA ATA TTC AGA GTT GAG AGT CAA AAG AGG GAC TCC TTC CAC AGA TCT AGT TTC AGG AAA
pro ile phe arg val glu ser gln lys arg asp ser phe his arg ser ser phe arg lys

2941                                                3001
TGT GAA ACC CAG TTG TCA CAG GGC AGC TAA GAA AAG CCA TCT TCA TTC GTG GAG ACT GTG
cys glu thr gln leu ser gln gly ser OCH

     ref 5.1
3001                                                3061
GCC CTG CAA CCC TGG AGA AGG ACT TGC TGG TAC TTA AAA AAT GGG ACA TTT GCC ACC CAG

3061                                                3121
GAC TGA CTG TAC ACT CCC TGA TCA GCC AGC ACT CTG GAA GCT TTG GGA TCC CAG GAA CCA

3121                                                3181
TGG AAT TAT TCC CAA ATG GAC TCT GAC CAG ATT TTT GCC ATA CTG GGG GGT GGC GGG ATG

3181                                                3241
GAT GAT GAG TAC TTA GGT ATG ACT GTT TAT TTA TTA AAC TGT GTT TTT CCA CAA TGT ACC

3241                                                3301
AAA GAA GTT ATA AAT AAT TTT TAT TAT TGA TTG GGC AAT GAT TAT TTA TAT GAA AGA TGA

3301                                                3361
TTT TCT CTT GTT GAT ATT TGA ATT TAT TAA AGT AAC TCA AAT TGC CTG AGG AAA AAT GGA

3361                                                3421
AAA ATT ATC CAC TAG TTG ATT CAA ACT GAA TTT CAC TCT TTA TAG GAA GGC AGG GCA AAC

3421                                                3481
TTT TAT AAT TAT GAA ATA TTT TTA ATA AAT TTA TAA AAG GAA TTT TTA TTA GAA TTT GAA
```

FIG. 4A (4 of 7)

```
                                                                    ...
AAA TCA TTA TGT TTG GAA ATT TGG GAG GAG ATT ATT TGT GAA GTT GTT ACC GTT TTG GTA

3541                                                        3571
ATG GTG GAT TAA TTA CTG TAT AGT TAT TTT TGT TTT ATT ATT ATT GTT ACA TTA ATT TAA

3601                                                        3631
CAT GCA TTT ATA GAA GAA TAC ATT CAA AGC ACT GAT GTA GGA GAT ACA CGG TAC TTG GAG

3661                                                        3691
CAG TCA GCC AAA AAT CAC AGA TAC TGC TTT CAC TTA AAT GGA TAC AAT TCT CCG ATA ATG

...                                                         3751
CTT TGC TTT TTT TCT TAT GTC ACT CTT GTG TAC TAT CTA TTT ITC TCC TCT CTG GGA CCA

3781                                                        3811
ACT TTT TTT TTA TAA AGC AAT AAT ATC TCT GTT TTC ATT TCA GAA CAT TGT GCT GTC TGT

3841                                                        3871
CAG CAT ATG TAT ATC AGC TAC AAA ATA TAT TCA ACT TTG ACT TCT TTT GAC AAA GGA CTT

3901                                                        3931
TAG GAA AAG GAG GAA CAA AGA CAT TAT TTG AGA ATT AAA TTA TAT ATT TTT AAT ATG ACT

3961                                                        3991
GTG AGC TTG AGT GAT AAT AAA TAT GTA ATA AGA ATT GCA AGC TAA AAA AAA AAA AAA AAA

4021
AAC TCG
```

Ref 1.1
Sequence of BAC19 using primer HC5S11, which spans nucleotides 3-22 of the cDNA.Exon sequence is underlined and represents nucleotides 32-57.

CTCTCTGTCTTCATATCTTCCAGGTTATAAAGNATTATTTACTAAAAGAANATTCANGC
TATTTCATTTAACTAGCTCAGTTTAATCATGTATTTCCTATAAAGGTTAGTCTTATTAAT
TTGACAAAACAATCAAACAATTCAAACCAGATCAAGTATGCTACCCTGAAGTTACACC
ACTAGTTAAGAATTAACAATCTAAGTAATTGGTTTCTCCCCAGGCTCAAGGCTCCCTGA
TTAGCTTAAGTAAAGCCAACAATCCAATAAGCCCTATGAAATTTAGAAACTCATAGAA
AAGTTTTAAATTTTTTTTTTTCACATTAAGCAATTGTTATATTATGCAAATAGAGGATT
NCAACTAAATAAGTTTGGAACCTGTTTACCAGGTTTTTGCAGCAGNCCTCTAAGAGCTT
AACTGGTCATGCATTGAATGCCGAGAGCAAAGAGGAATGGAGAGGGGNTGTAAGNGG
TTCCAATNTTACTGGAACCCACCACTATCTTTNGAAGTCTTGATACTTAACTGNGTGTA
NNTTCTTTAGGCCTNTANTAANTAGAATCTATATCGATTCGTGTTCTGTCNGCAAGNAG
TGCCTATGAAA

FIG. 4A (5 of 7)

Ref 2.1

Sequence of BAC19 using primer HC5AS10b, which spans nucleotides 5??-58? of Exon sequence is underlined and represents nucleotides 510-553.

TGCGAGTAGTGTCCGCGTTCAGCATGTTGTACTGCTTATAGGGCTCAAGGGAGGCACG
ATTGGGGGATGGAGGCCAGGGAAGAAGTCAAGCAACAGAAAAATTTGAGGCTTAACA
GTCAAGCAACAGAAAAATTCAAACTGTTCTCTTAAAATACCATGACTGTACATCACTG
CTAGGCTGGAGATCTATTGCCAGTAGCTCTGCCTTCCCTAGGCAGGGGAAGCTGTGTT
CTTTGAGTAGCGCCACTCAGCAAAGAGCCTCACCTGGGCAGTATTTGAGCTAGGCTT
TCAGCCACCGTACCTGAGTACCTCTGTTTTANGAGCAGTGTGGCCTGGTGATCACCCT
GGGCCTTGATCATGCGTGCTGCAATCCTAGTGATACAAAGAGGCTTCATGCTGCTAA
GATCTCCAAGTATTTTTCCTTCGTGCTGGGCATCAGAGGGTTAGACTTNCAGGGGAGA
AGGAAACTGGCTGGGTGCCATGAATAANCTTGCTGTTCAAGANTTAACTTCTTTGTTAC
ATAAGNGCAAAGGTATAACATAAACGGNCATGAACTGCTCAACNAAATTNATCAAAT
CCATGTTTGTGGCAGTTCTTTTGTNATNGGAAGTTTAACCCCTAA

Ref 3.1

Sequence of BAC19 using primer C5S3, which spans nucleotides 10?6-1115 of the cDNA. Exon sequence is underlined and represents nucleotides 1110-1120.

CCCNGCTCTTTTTGCCAANGTAANCTTGGGATGCTTGTTTTCTTCCTCTTAATTAAGAG
NAAGANTTTTTTTAGCTTCATACTTCTCTCTTCAGGGGGACCAAAAGTCACAGAGCATA
TTAAGTGGCANAACCCCNAAGGTCTTAAGTCTTCCCTAGGAAGAAAGCAGATGCCCTGA
TTCTGTGGAAGCCACCATGGAGAGGAAAAGCAGTGGCTCCCATATTTGAAGTGNGGA
CCTAACTCTAGAAAGTTTAAAANGGCCATTTGCTGAAGGGCTATGACATGAGAACAGA
GATCAACTGAGTGACTTAGCAANTTCACTCTTTCTCTGTAANACCTCTGGTGAGTGAGA
NTAAATCCTNTATGTGACGCCCATTAGTCTTACAAAANGTCATGCCNTAAAATGCCAN
GAAGGNCAGAAATGAATTTCTCACCGCCNGAGGAATGAGGATTATNCTGGGGGGACA
TGCANAAATATTNNCCCCCNATTTATTNATTTATTTATTTTTGAGACNGAGTNTCGNT
CTAATCGCCCCCAGGCTGGNAGGTGGNAGGTGGTTCCCATCTTNAANCTTANNTNGGA
AGGNCCTCTTTGNGCCCCNGGGGGNGNAAAGNGAATTCCCTAAATGCCTNCANNCCCC
TCCCTGGANGTTATTTGGGGGNNTTNTAAAGGGCNGTGGCNG

Ref 4.1

Sequence of BAC13 using primer C5S7, which spans nucleotides 11?6-2206 of the cDNA. . Exon sequence is underlined and represents nucleotides 22??-2231.

ATNNNNATTNACTAACANTCTTTAANTCCCAACANTCTTTTTTTAAGAATACCTAANG
ATTTTNACTNNGGCTTATTTCTCAANGCATTAAAAGCAGNCAAACNACNCCNNCAAG
AGNGGCAACTACTAATGGGGCANATCTNAAAGAAAATATAGNCAAAGGNNGGAATCA
TAATAGGAGCNACTACTTANGAAGCACCAACTGGGGACCTGGAACTGNATNAGGNCC
TCTACATACATCATNNNATANCATCCTGCAACGACCCCTGGAAGGAGANAGANGGNA
TTCCTANNNTAGATANGAGANAACTGGGGACATGGAAGAGGNAAGCGAAGGGTTCA
AGGGGANGNAACCCAGCAGANNCCAGGGNCTCANACTNGNGGGGNNTGGGGGGNTN
CTGNNNCCCTACNCTTNGNANGAACAGNGNNGTTGANNTGGCTTTNGANTA

[illegible]

FIG. 4A (6 of 7)

CCANNAGATTNTTGNAACGNNGGTAGGCTTCCTTTGTAGATTTATTGAAAATGTTTCGT
ACTTCTACAAGTTTGCCCTGCCTTCCTATAAAGAGTGAAANTCANTTTGAATCGACTGG
TGGATAATTNTTCCATTTTTCCTCAGGCAATTTNGAGTTACTCCAATAAATTCAAATAT
GGGCCAGAGGAAATCATCTTTCAGATGGGCAGTGATTGGCCAGTCAGCAGGAGAAGC
TGCTTATGCCTTGTTTGGTACATTGTGGAAAAACACACTTTAATAAATACGCANTCATG
CCTGAGTACCCATCCTCCATCCCGCCACCCCCCAGTATGGCAAAAATCTGGTCAGAGT
CCATTTGGGAATAATTCCATGGTTCCTGGGATCCCAAAGCTTCCAGAAGTGCTGGCTG
ATCAANGGAGTGTACAGTCAGTCCTGCGTGGCAAAAATGTCCCATTTTTTAAGTACCA
AGCAAAGGTTCCTTCTTNCAAGGGTTNCTAGGGCC

FIG. 4A (7 of 7)

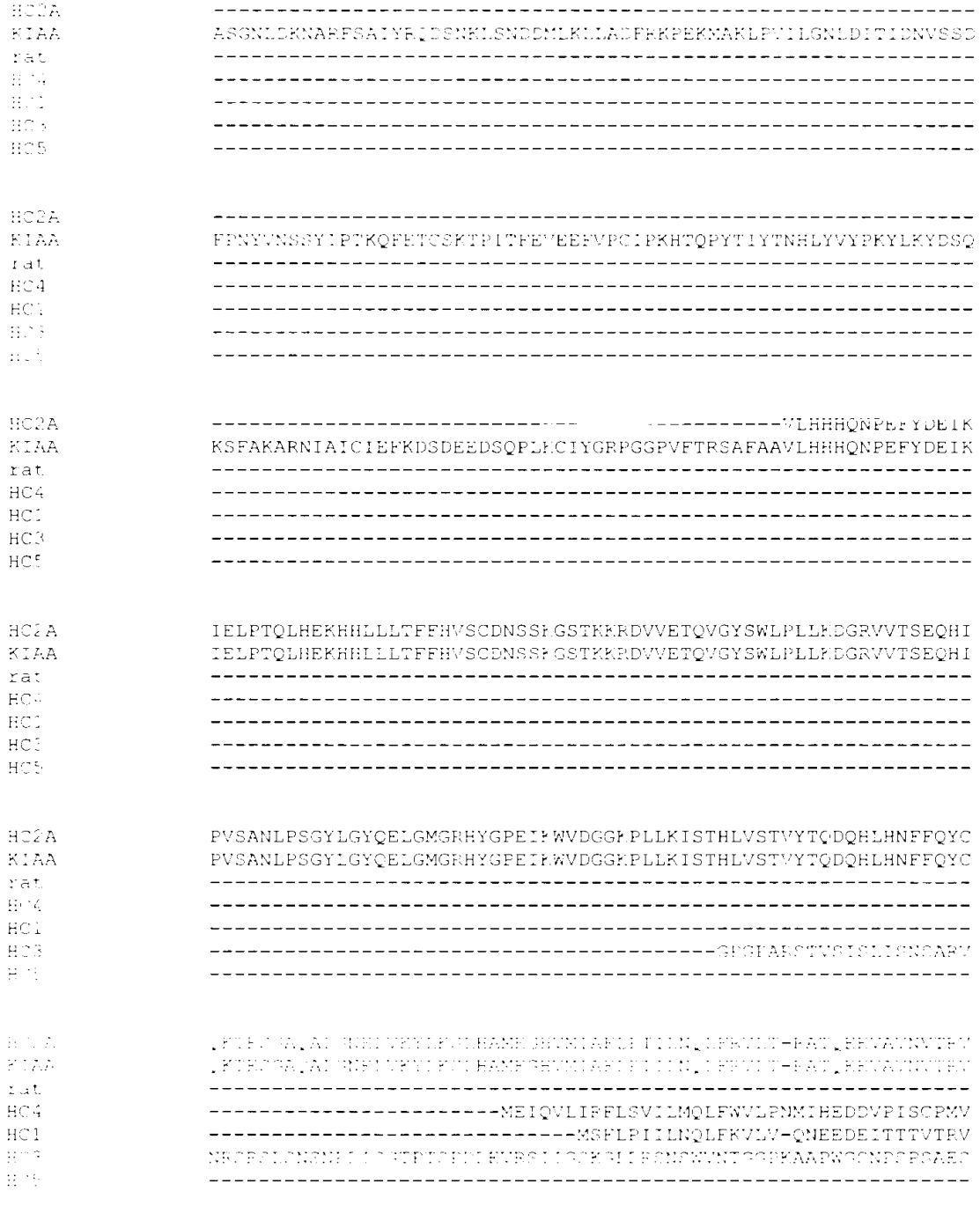


FIG. 4B (1 of 5)

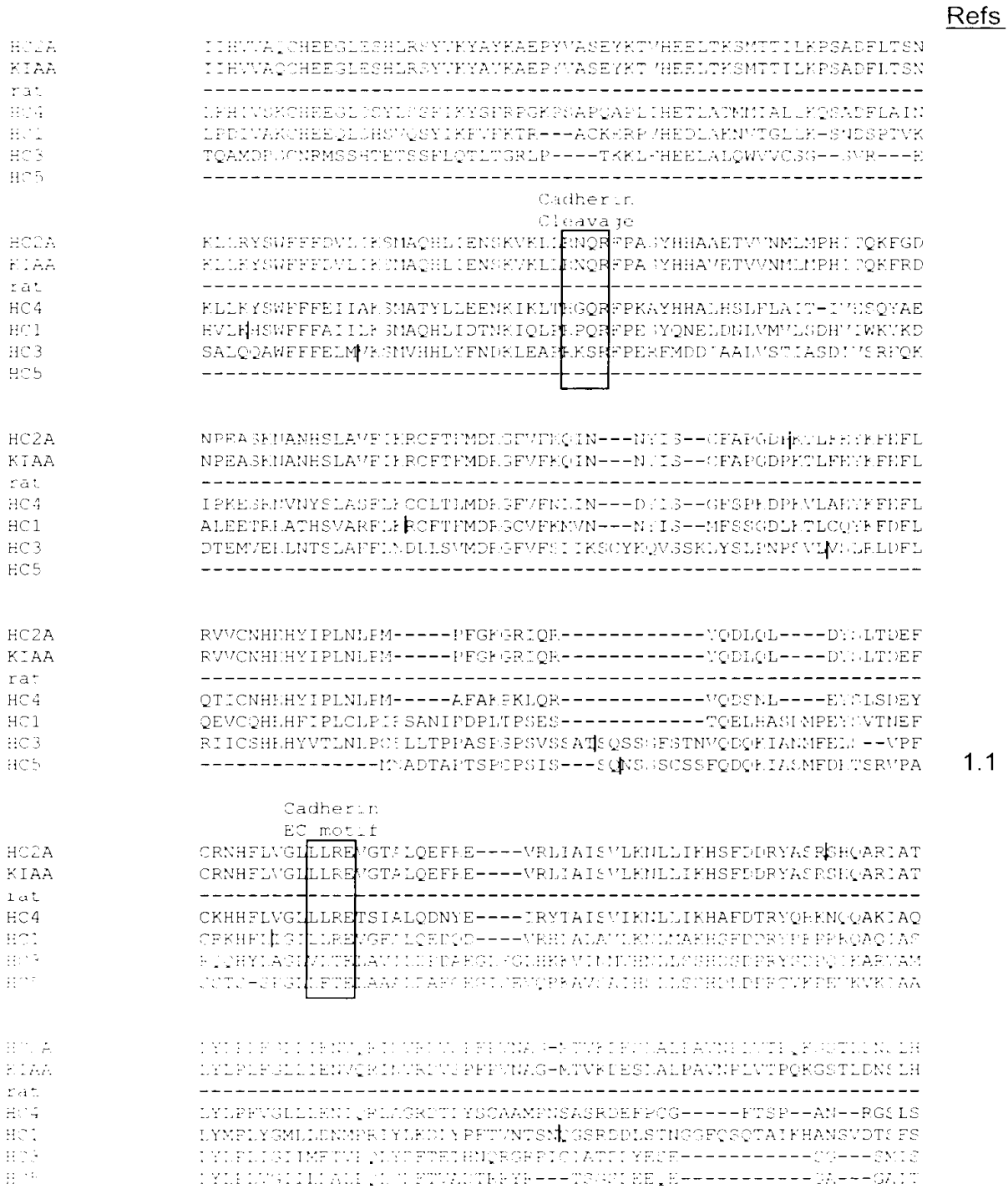


FIG. 4B (2 of 5)

FIG. 4B (3 of 5)

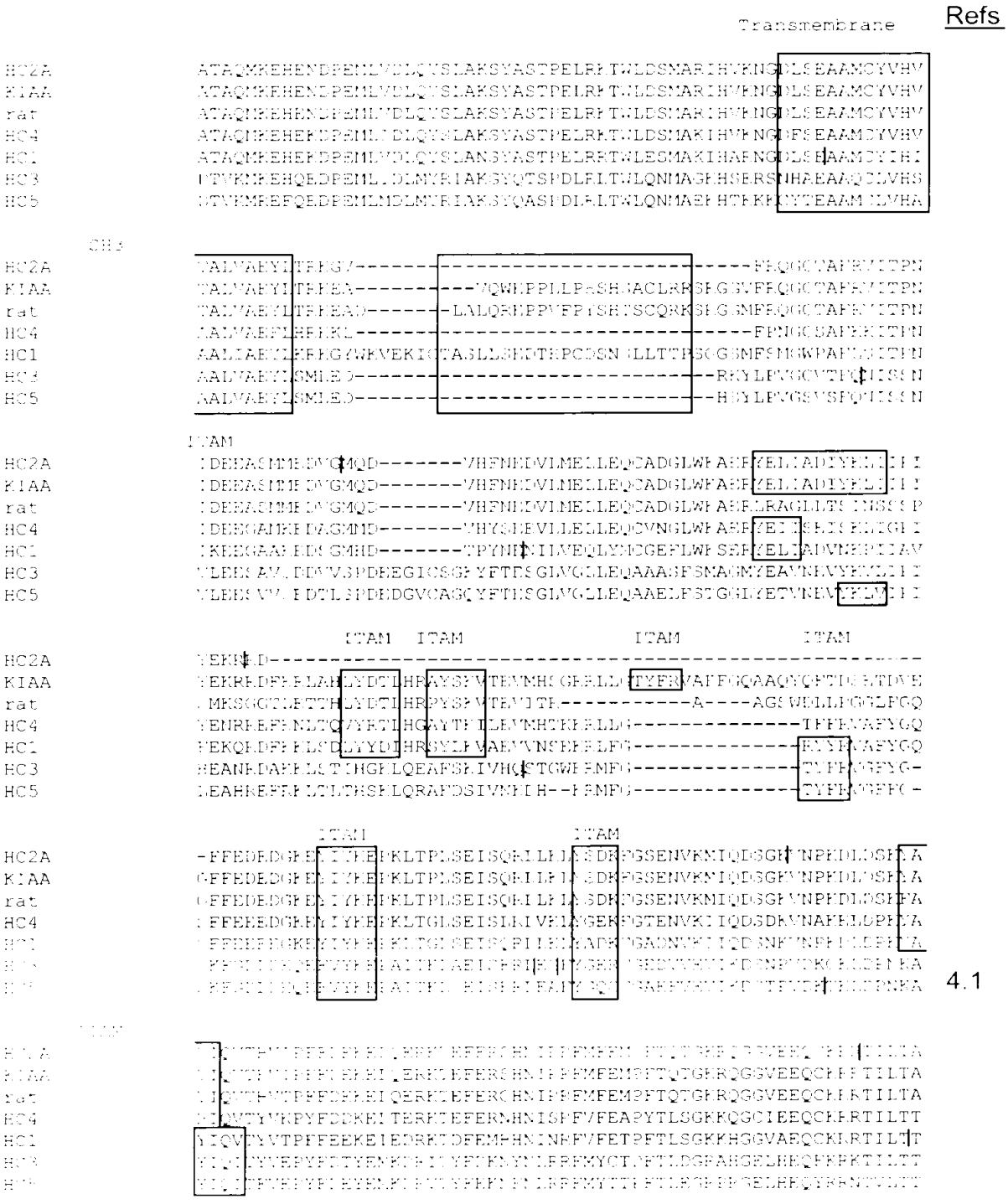

Transmembrane
Refs
HC2A
KIAA
rat
HC4
HC1
HC3
HC5
ITAM
ITAM
ITAM
ITAM
ITAM
ITAM
4.1

FIG. 4B (4 of 5)

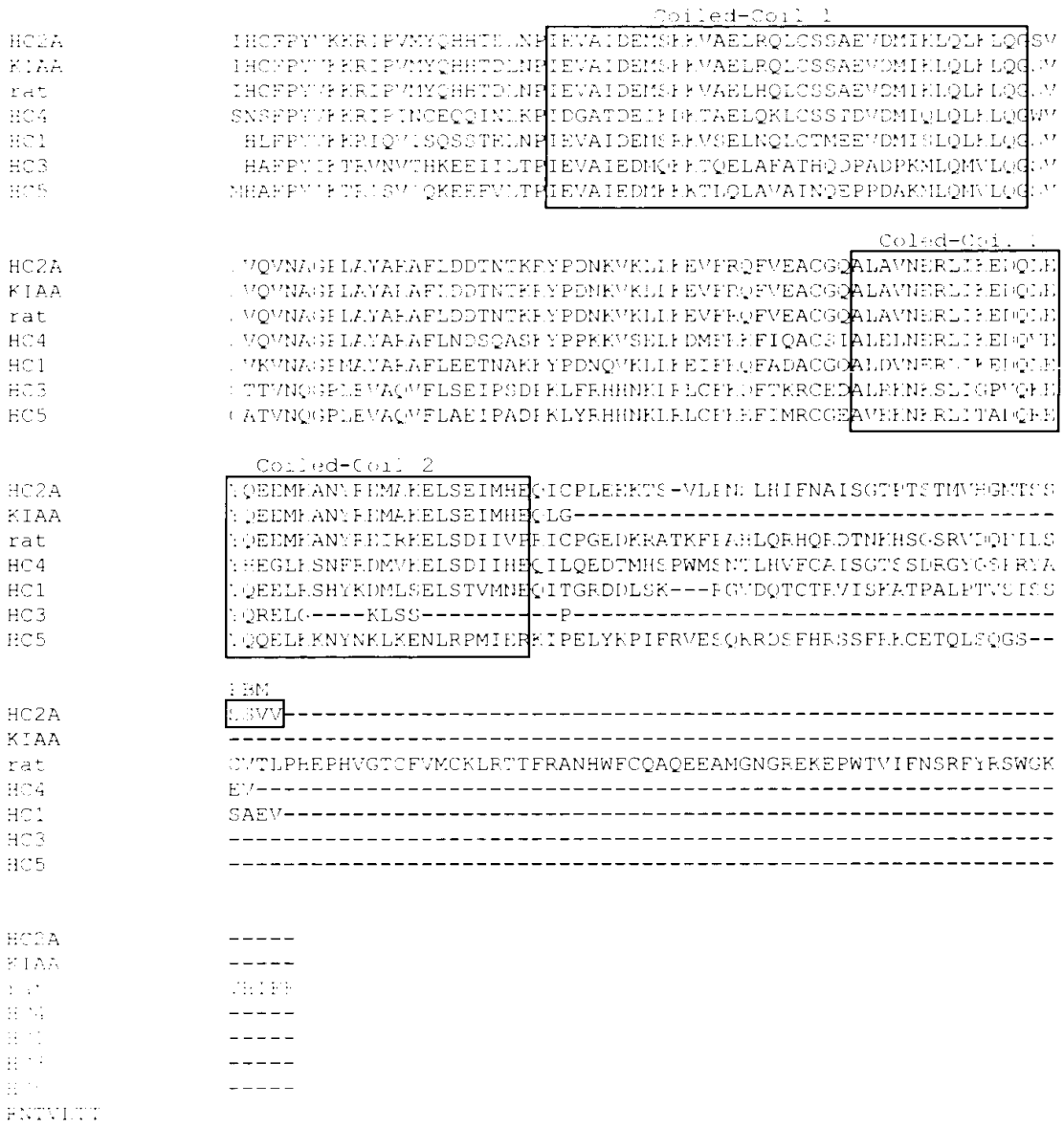

Coiled-Coil 1
Coiled-Coil 1
Coiled-Coil 2
IBM
HC2A
KIAA
rat
HC4
HC1
HC3
HC5

FIG. 4B (5 of 5)

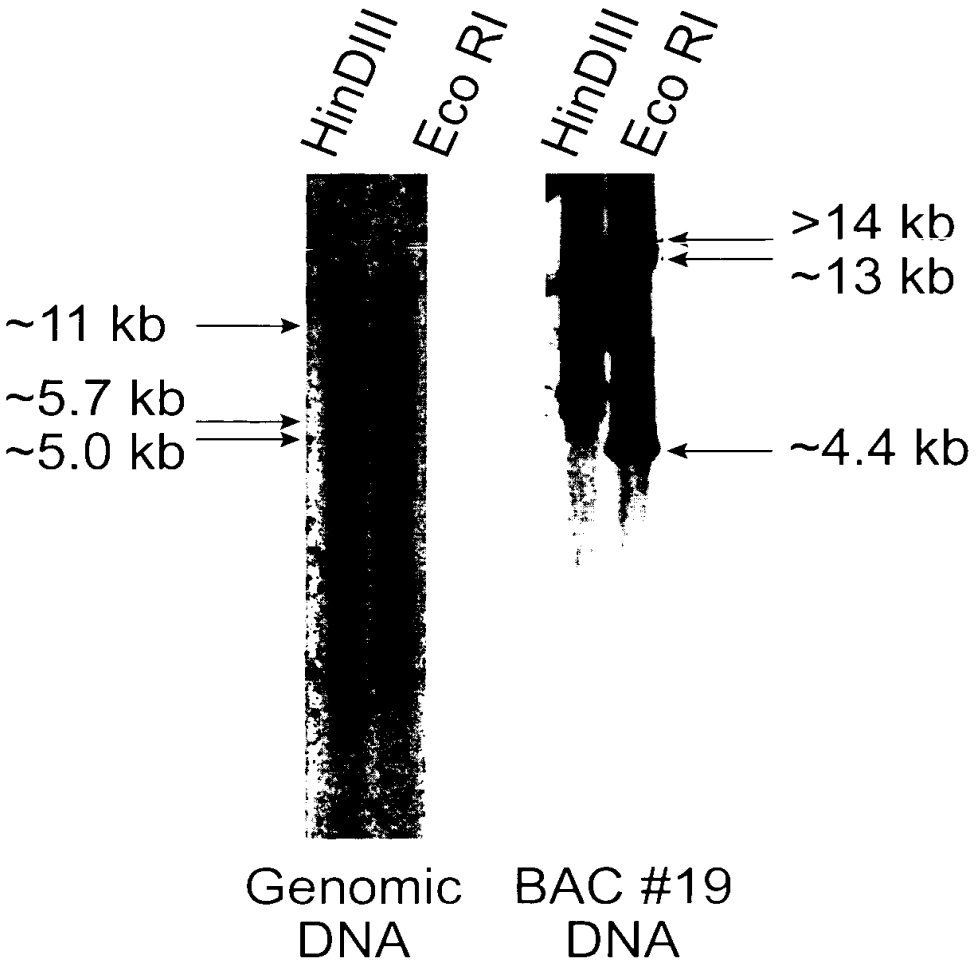

HinDIII
Eco RI
HinDIII
Eco RI
>14 kb
~13 kb
~11 kb
~5.7 kb
~5.0 kb
~4.4 kb
Genomic DNA
BAC #19 DNA

FIG. 5

-111

CGGTAACCGCCATTTTGTCTCCTGTAACAATTTACGCGCCGTGTAACTGTGAATCTTTCAAAGCCTCAGTTTTATGACC

CTGTGGAGTCAGTGGACTTTGAAGGACTTCTG -1

1/1 31/11

ATG ACA CAC CTG AAC AGC CTG GAT GTG CAG CTT GCC CAG GAG CTC GGG GAC TTC ACT GAT

met thr his leu asn ser leu asp val gln leu ala gln glu leu gly asp phe thr asp

61/21 91/31

GAC GAC TTG GAC GTG GTG TTC ACG CCA AAG GAA TGT AGG ACT TTG CAG CCC TCT TTG CCG

asp asp leu asp val val phe thr pro lys glu cys arg thr leu gln pro ser leu pro

121/41 151/51

GAG GAA GGG GTT GAA CTG GAC CCT CAT GTC AGG GAC TGT GTT CAG ACC TAC ATC CGT GAG

glu glu gly val glu leu asp pro his val arg asp cys val gln thr tyr ile arg glu

181/61 211/71

TGG CTA ATC GTG AAC CGG AAA AAC CAA GGA AGT CCA GAA ATC TGT GGC TTT AAA AAG ACT

trp leu ile val asn arg lys asn gln gly ser pro glu ile cys gly phe lys lys thr

241/81 271/91

GGA TCT CGA AAA GAT TTT CAC AAG ACG CTT CCG AAA CAG ACG TTT GAG TCG GAA ACC TTG

gly ser arg lys asp phe his lys thr leu pro lys gln thr phe glu ser glu thr leu

301/101 331/111

GAG TGC AGT GAA CCC GCT GCT CAG GCA GGC CCC CGC CAC TTA AAC GTG CTG TGC GAC GTG

glu cys ser glu pro ala ala gln ala gly pro arg his leu asn val leu cys asp val

361/121 391/131

TCT GGG AAA GGC CCC GTC ACT GCC TGT GAC TTT GAC CTC CGC AGC CTG CAG CCT GAC AAG

ser gly lys gly pro val thr ala cys asp phe asp leu arg ser leu gln pro asp lys

421/141 451/151

CGG CTA GAA AAC CTC CTG CAG CAA GTG AGT GCC GAG GAC TTT GAG AAG CAG AAC GAG GAG

arg leu glu asn leu leu gln gln val ser ala glu asp phe glu lys gln asn glu glu

481/161 511/171

GCC CGG AGG ACC AAC AGG CAG GCC GAG CTC TTT GCC CTT TAC CCA TCA GTG GAC GAG GAG

ala arg arg thr asn arg gln ala glu leu phe ala leu tyr pro ser val asp glu glu

541/181 571/191

GAT GCT GTG GAA ATA CGT CCA GTA CCA GAA TGT CCC AAG GAA CAC CTG GGC AAC AGA ATA

asp ala val glu ile arg pro val pro glu cys pro lys glu his leu gly asn arg ile

601/201 631/211

TTG GTC AAG TTG CTG ACC TTG AAG TTC GAG ATT GAA ATT GAG CCC CTG TTT GCC AGC ATT

leu val lys leu leu thr leu lys phe glu ile glu ile glu pro leu phe ala ser ile

661/221 691/231

GCC CTC TAC GAT GTT AAA GAA AGG AAA AAG ATC TCA GAA AAT TTT CAC TGT GAC CTG AAC

ala leu tyr asp val lys glu arg lys lys ile ser glu asn phe his cys asp leu asn

721/241 751/251

TCT GAT CAG TTT AAA GGA TTT CTG CGA GCT CAC ACG CCT TCA GTG GCT GCA TCA AGT CAG

ser asp gln phe lys gly phe leu arg ala his thr pro ser val ala ala ser ser gln

781/261 811/271

GCA AGA TCT GCA GTC TTT TCA GTC ACA TAC CCT TCT TCA GAC ATC TAC CTG GTA GTT AAG

ala arg ser ala val phe ser val thr tyr pro ser ser asp ile tyr leu val val lys

841/281 871/291

ATT GAA AAA GTT CTG CAG CAG GGA GAT ATT GGA GAC TGT GCA GAG CCC TAC ACG GTT ATC

ile glu lys val leu gln gln gly asp ile gly asp cys ala glu pro tyr thr val ile

901/301 931/311

AAA GAA AGT GAT GGT GGA AAC AGT AAA GAA AAG ATT GAA AAA CTA AAA CTC CAA GCT GAA

lys glu ser asp gly gly lys ser lys glu lys ile glu lys leu lys leu gln ala glu

961/321 991/331

[illegible]

FIG. 6A (1 of 6)

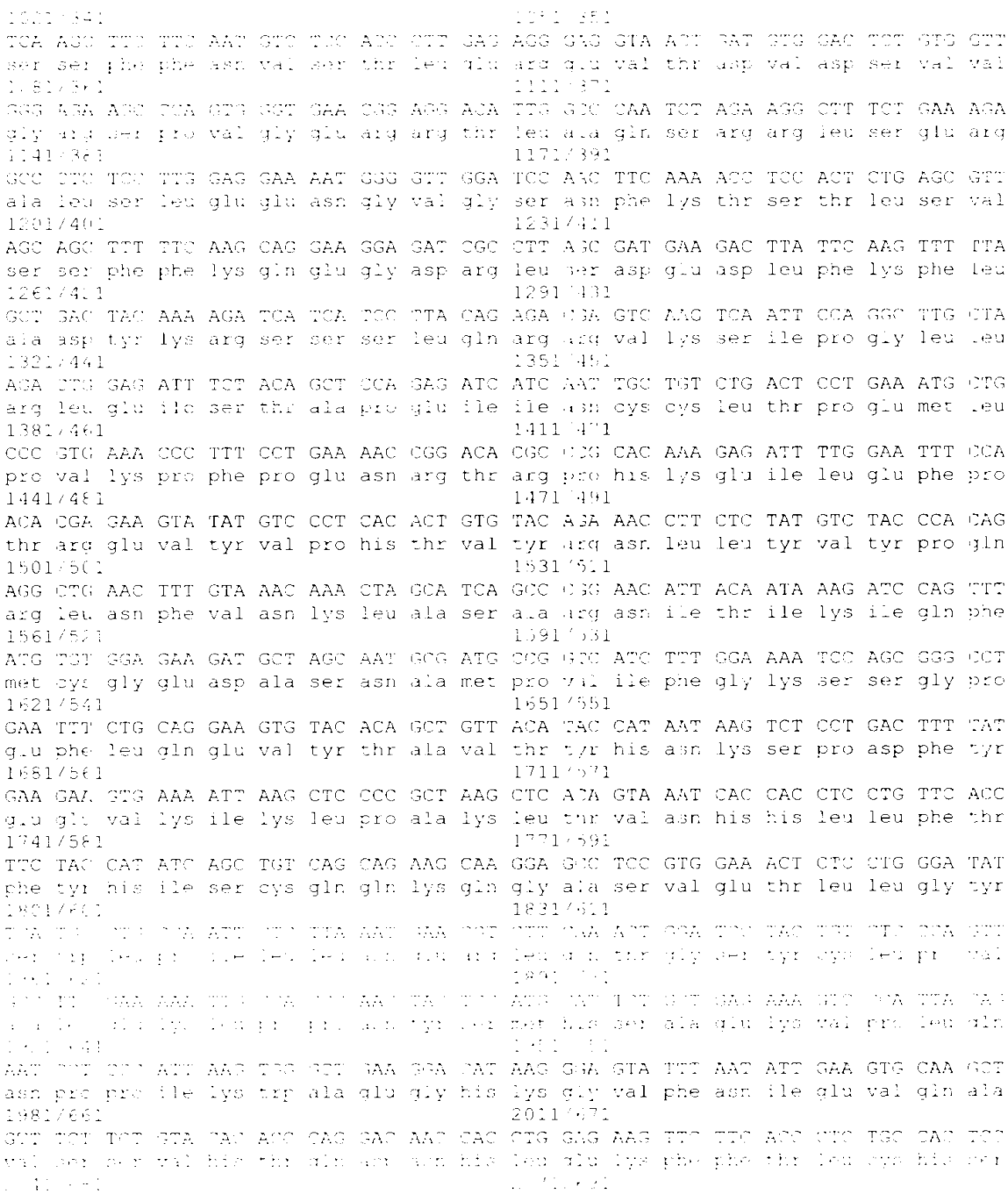


FIG. 6A (2 of 6)

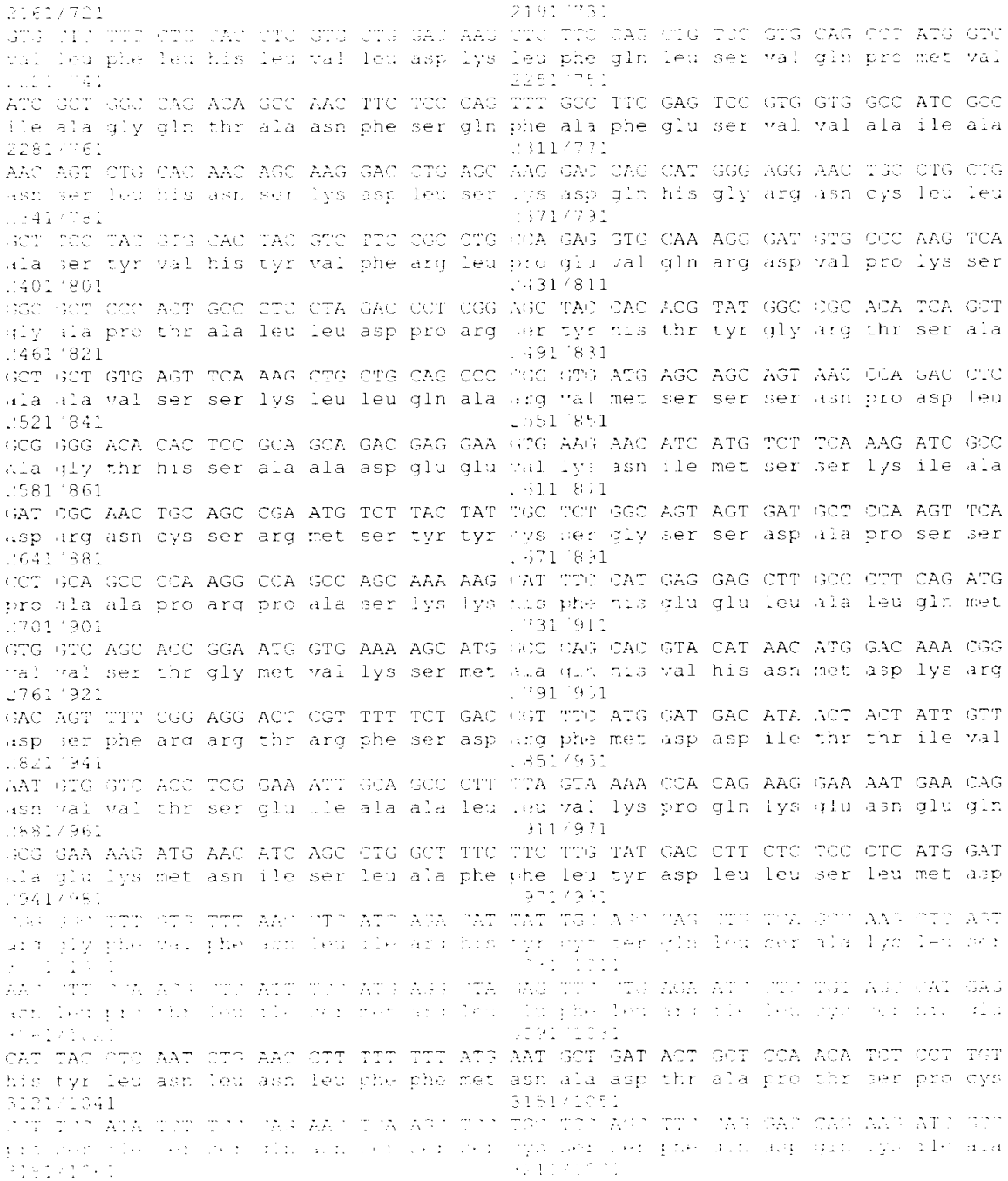


FIG. 6A (3 of 6)

3301/1101 3331/1111
GCT GTC AGT GCA ATT CAC AGC CTG CTA AGT TCT CAC GAC CTG GAC CCA CGC TGT GTC AAA
ala val ser ala ile his ser leu leu ser ser his asp leu asp pro arg cys val lys
3361/1121 3391/1131
CCA GAG GTG AAG GTC AAA ATC GCC GCC CTT TAC CTA CCT TTA GTT GGC ATC ATT TTG GAT
pro glu val lys val lys ile ala ala leu tyr leu pro leu val gly ile ile leu asp
3421/1141 3451/1151
GCT TTG CCA CAG CTC TGT GAC TTT ACA GTT GCA GAT ACT CGC AGA TAC CGC ACC AGT GGC
ala leu pro gln leu cys asp phe thr val ala asp thr arg arg tyr arg thr ser gly
3481/1161 3511/1171
TCG GAT GAA GAA CAA GAA GGA GCC GGT GCC ATT AAC CAG AAT GTG GCT CTG GCC ATA GCA
ser asp glu glu gln glu gly ala gly ala ile asn gln asn val ala leu ala ile ala
3541/1181 3571/1191
GGG AAT AAT TTC AAT TTG AAA ACA AGT GGA ATA GTG CTG TCT TCC TTG CCC TAT AAG CAG
gly asn asn phe asn leu lys thr ser gly ile val leu ser ser leu pro tyr lys gln
3601/1201 3631/1211
TAC AAC ATG CTG AAC GCG GAC ACT ACT CGC AAC CTC ATG ATC TGC TTC CTC TGG ATC ATG
tyr asn met leu asn ala asp thr thr arg asn leu met ile cys phe leu trp ile met
3661/1221 3691/1231
AAA AAT GCT GAT CAG AGC CTC ATT AGG AAG TGG ATT GCT GAC CTG CCA TCA ACG CAG CTC
lys asn ala asp gln ser leu ile arg lys trp ile ala asp leu pro ser thr gln leu
3721/1241 3751/1251
AAC AGG ATT TTA GAT CTA CTT TTC ATC TGT GTG TTA TGT TTT GAG TAT AAG GGA AAA CAG
asn arg ile leu asp leu leu phe ile cys val leu cys phe glu tyr lys gly lys gln
3781/1261 3811/1271
AGT TCT GAC AAA GTC AGT ACC CAA GTC CTG CAG AAG TCA AGG GAT GTC AAG GCC CGG CTG
ser ser asp lys val ser thr gln val leu gln lys ser arg asp val lys ala arg leu
3841/1281 3871/1291
GAA GAG GCT TTG CTG CGT GGG GAA GGG GCC AGA GGG GAG ATG ATG CGC CGC CGG GCT CCA
glu glu ala leu leu arg gly glu gly ala arg gly glu met met arg arg arg ala pro
3901/1301 3931/1311
GGG AAC GAC CGA TTT CCA GGC CTA AAT GAA AAT TTG AGA TGG AAG AAA GAG CAG ACA CAT
gly asn asp arg phe pro gly leu asn glu asn leu arg trp lys lys glu gln thr his
3961/1321 3991/1331
TGG CGG CAA GCT AAT GAG AAG CTA GAT AAA ACA AAG GCC GAG TTA GAT CAA GAA GCC TTG
trp arg gln ala asn glu lys leu asp lys thr lys ala glu leu asp gln glu ala leu
4021/1341 4051/1351
ATC AGT GGC AAT CTG GCT ACA GAA GCA CAT TTA ATC ATC CTG GAT ATG CAG GAA AAC ATT
ile ser gly asn leu ala thr glu ala his leu ile ile leu asp met gln glu asn ile
4081/1361 4111/1371
ATC CAG GCG AGC TCG GCT CTG GAC TGT AAA GAC AGC CTG CTG GGA GGT GTT CTG AGG GTG
ile gln ala ser ser ala leu asp cys lys asp ser leu leu gly gly val leu arg val
4141/1381 4171/1391
[illegible] AAT [illegible] AAT [illegible] GAT CAG [illegible] TAC [illegible] TTT [illegible]
leu val asn ser leu asn tyr asp gln ser thr thr tyr leu thr [illegible] cys phe ala thr
4201/1401 4231/1411
[illegible] AAA [illegible] GAA GAG GTG GAA CAG TGT
leu arg ala leu ile ala lys phe gly asp leu leu phe glu glu glu val glu gln cys
4261/1421 4291/1431
TTC GAC CTA TGT CAC CAA GTC CTG CAT CAC TGC AGC AGC AGC ATG GAT GTC ACC CGG AGC
phe asp leu cys his gln val leu his his cys ser ser ser met asp val thr arg ser
4321/1441 4351/1451
CAA [illegible] ATG AGG TTC AGT TTT [illegible] ACC AGT AAT TTT
[illegible]

FIG. 6A (4 of 6)

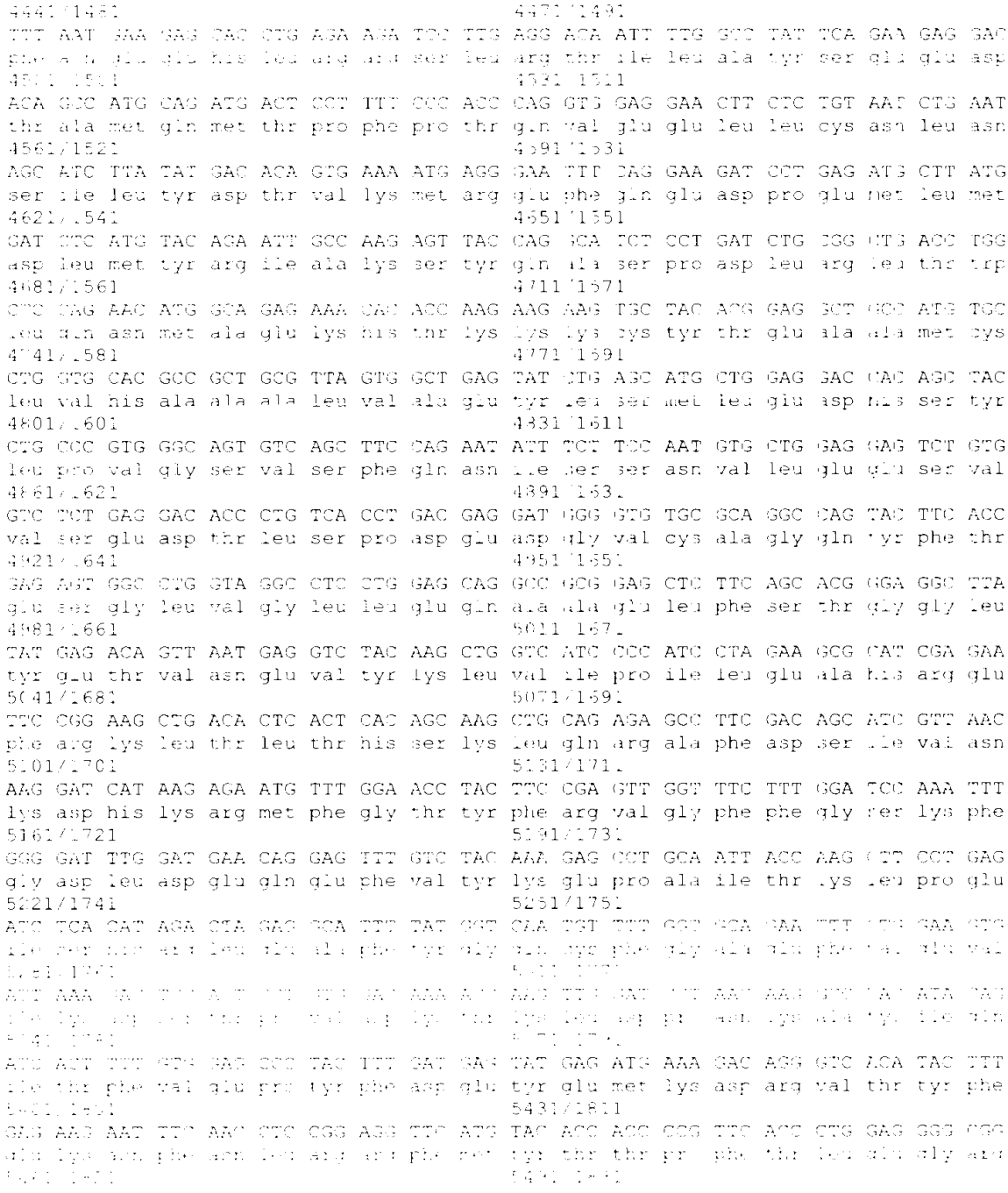


FIG. 6A (5 of 6)

5581/1861 5611/1871
ATT GAA GTT GCT ATT GAA GAC ATG AAG AAG AAG ACC CTG CAG TTA GCA GTT GCC ATT AAC
ile glu val ala ile glu asp met lys lys lys thr leu gln leu ala val ala ile asn
5641/1881 5671/1891
CAG GAG CCG CCT GAT GCA AAG ATG CTT CAG ATG GTG CTG CAA GGC TCT GTG GGA GCT ACT
gln glu pro pro asp ala lys met leu gln met val leu gln gly ser val gly ala thr
5701/1901 5731/1911
GTA AAT CAG GGA CCA CTG GAA GTA GCC CAA GTG TTT TTG GCT GAA ATT CCT GCT GAT CCA
val asn gln gly pro leu glu val ala gln val phe leu ala glu ile pro ala asp pro
5761/1921 5791/1931
AAA CTC TAT CGA CAT CAC AAC AAG TTG AGG TTA TGC TTT AAG GAA TTC ATC ATG AGA TGT
lys leu tyr arg his his asn lys leu arg leu cys phe lys glu phe ile met arg cys
5821/1941 5851/1951
GGT GAA GCT GTA GAG AAA AAC AAG CGT CTC ATC ACG GCA GAC CAG AGG GAA TAT CAG CAG
gly glu ala val glu lys asn lys arg leu ile thr ala asp gln arg glu tyr gln gln
5881/1961 5911/1971
GAA CTC AAA AAG AAC TAT AAC AAG CTA AAA GAG AAC CTC AGG CCA ATG ATC GAG CGG AAA
glu leu lys lys asn tyr asn lys leu lys glu asn leu arg pro met ile glu arg lys
5941/1981 5971/1991
ATT CCA GAA CTG TAC AAG CCA ATA TTC AGA GTT GAG AGT CAA AAG AGG GAC TCC TTC CAC
ile pro glu leu tyr lys pro ile phe arg val glu ser gln lys arg asp ser phe his
6001/2001 6031/2011
AGA TCT AGT TTC AGG AAA TGT GAA ACC CAG TTG TCA CAG GGC AGC TAA
arg ser ser phe arg lys cys glu thr gln leu ser gln gly ser OCH

GAAAAGCCATCTTCATTCGTGGAGACTGTGGCCCTGCAACCCTGGAGAAGGACTTGCTGGTACTTAAAAAATGGGACATT
TGCCACCCAGGACTGACTGTACACTCCCTGATCAGCCAGCACTCTGGAAGCTTTGGGATCCCAGGAACCATGGAATTATT
CCCAAATGGACTCTGACCAGATTTTTGCCATACTGGGGGGTGGCGGGATGGAGGATGGGTACTCAGGCATGACTGCGTAT
TTATTAAAGTGTGTTTTTTCCACAATGTACCAAACAAGGCATAAGCAGCTTCTCCTGCTGACTGGCCAATCACTGCCCATC
TGAGAGATGATTTCCTCTGGCCCATATTTGAATTTATTGGAGTAACTCAAATTGCCTGAGGAAAAATGGAAAAATTATCC
ACCAGTCGATTCAAACTGAATTTCACTCTTTATAGGAAGGCAGGGCAAACTTGTAGGAGTACGAAACATTTTCAATAAAT
CTACAAAGGGAAGCCTTACTACAATTCCAAAAATCATCATGGTTGGAAATTTGGGAGGAGATTATTTGTGAACTTGTTAC
CCTTTTGGTAATGGTGGACTAATTGCTGTATAGTTATTTTTGTTTTATTATTACTGTTACATTAATTTAACATGCATTTA
TAGAAGAATACATTCAAAGCACTGATGTAGGAGATACACGGTACTTGGAGCAGTCAGCCAAAAATCACAGATACTGCTTT
CACTTAAATGGAAACAATTCTCCGATAATGCTTTGCTTTTTTTCTTATGTCACTCTTGTGTACTATCTATTTTTCTCCTC
TCTGGGACCAAGTTTCTTTTTATAAAGCAATAATATCTCTGTTTTCATTTCAGAACATTGTGCTGTCTGTCAGCATATGT
ATATCAGCTACAAAATATATTCAACTTTGACTTCTTTTGACAAAGGACTTTAGGAAAAGGAGGAACAAAGACATTATTTG
AGAATTAAATTATATATTTTTAATATGACTGTGACCTTGACTGATAATAAAGATGTAATAAGAATTGCAAGCTAAAAAAA
AAAAAAAAAAAACTCG

FIG. 6A (6 of 6)

A. Allelic variations: single nucleotide changes (polymorphism) between CLASP-5 cDNA isoforms

Isoform	Nucleotide(s)	Consequence
1	1727	C to T change; mis-sense mutation changing codon from alanine to valine
2	1749	A to G change; silent mutation
3	2277	G to C change; silent mutation
4	2853	C to T change; silent mutation
5	3427	A to G change; mis-sense mutation changing codon from lysine to glutamic acid
6	3777	C to T change; silent mutation

B. Alternative splices

Isoform	Difference	Nucleotide(s)	Consequence
1	exon deletion	1806-1944	premature, in-frame stop codon leading to the production of a truncated, most likely soluble protein
2	exon insertion	between 2857 and 2858	additional, in-frame 48 nucleotide exon that contains a stop codon at the second codon, which would lead to a truncated, most likely soluble protein

These differences may be found separately or together in various combinations in the different human CLASP-5 isoforms

FIG. 6B

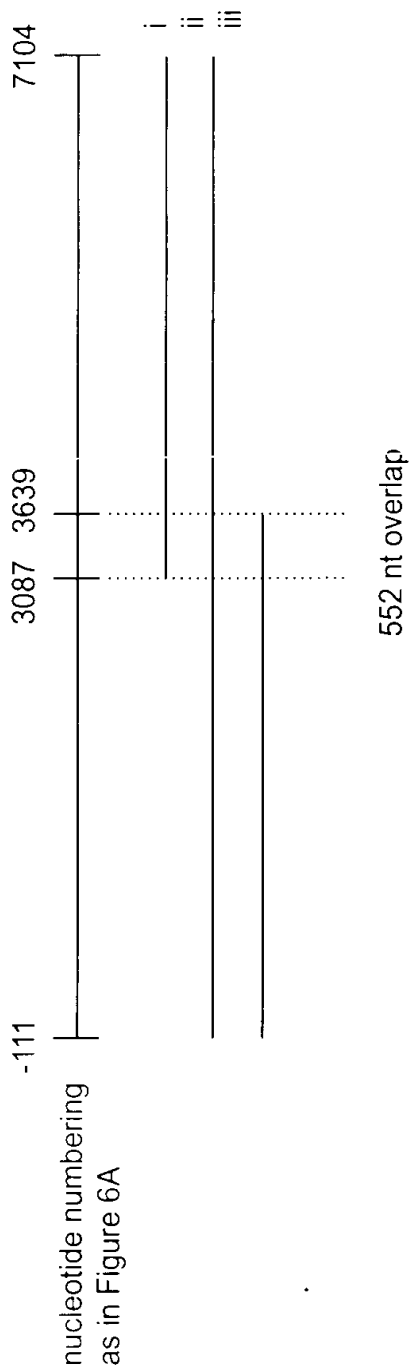

7104
3639
3087
-111
i
ii
iii
552 nt overlap
nucleotide numbering
as in Figure 6A

FIG. 6C

1st partial exon (nucleotides 3793 to 3952)
CCAGCTGTCAGCCAAGCTCAGTAACCTTCCAACGCTCATTTCCATGAGGCTAG
AGTTCCTGAGAATCCTCTGTAGCCATGAGCAATTACCTCAATCTGAACCTTTTT
TTTATGAATGCTGATACTGCTTCCAACATCTCCTTGTCCTTCCATATCTTCCCAG
GTAATAAAAGAATTATTTAACTAAAAGAATTATTCAAGCTAT

2nd exon (nucleotides 5909 to 5948)
GCTCATAAAATGGCTCCTTACGTTTCTGTAGAACTCAAGCTCCTGCTCCAGCT
TGCAGGACCAGAAGATCGCCAGCATGTTCGATCTGACTTCCGAGTACCGCCA
GCAGCACTTCCCTCACCGGGCTCCTGTTCACAGAACTGGCTGCTGCCCTGGATG
CCGAAGGGAAGGGTATGTTTCTGGCATTTAAAATGGAAGATGAAGC

3rd exon (nucleotides 13662 to 13831)
CATAACCTCTTGATTCCTGTGTTGTGCCAACAGAATCAGCAAAGTACAAAGG
AAAGCTGTCAGTGCAATTCACAGCCTGCTAAGTTCTCACGACCTGGACCCA
GCTGTGTCAAACCAGAGGTGAAGGTCAAAATGGCCGCCCTTTACCTACCTTTA
GTTGGCATCATTTTGGATGCTTTGCCACAGCTCTGTGACTTTACAGGTAATGG
CCCTTCTGTTTTCTTTCTTGGATTG

4th exon (nucleotides 16948 to 17087)
TGTTTGACTTGACATCACAAACGATGTTTTCATTGCAGTTGCAGATACTCGCA
GATACCGCACCAGTGGCCTCGGATGAAGAACAAGAAGGAGCCGGTGCCATTA
ACCAGAATGTGGCTCTGGCCATAGCAGGGAATAATTTCAATTTGAAAACAAG
TGGAATAGTGCTGTCTTCCTTGGTATGTTGGTGCACATGTGTCTGGTTGATTTT
TCAT

5th exon (nucleotides 19281 to 19463)
TGGCCTCCATCCCCCAATCTGCCTCCCTTCAGCCCTATAAGCAGTACAACATG
CTGAACGCGGGACACTACTGGCAACCTCATGATCTGCTTCCTCTGGATCATGAA
AAATGCTGATCAGAGCCTCATTAGGAAGTGGATTGCTGACCTGCCATCAACG
CAGCTCAACAGGATTTTACATCTACTTTTCATCTGTGTGTTATGTTTTGAGTAT
AAGGTAAGTCTGGAGTGGCACACTTTATACCAGC

6th exon (nucleotides 19829 to 19958)
CACCAAAGGACATGTCCTCCTACCTCTGTCTTGTCCAGGGAAAACAGAGTTCT
GACAAAGTCAGTACCCAAGTCCTGCAGAAGTCAAGGGATGTCAAGGCCCGG
CTGGAAGAGCCTTTGCTGCGTGGGGAAGGGGCCAGAGGGGCAGATGATGCGC
CGCCGGGCTCCAGGTGTGTTGGACTGGCCCTTGCCTGCTCTGTCAAGC

FIG. 7A (1 of 4)

7th exon (nucleotides 20929 to 21015)
TCAAATTCCTATCATCCATTTCTTAACTCCTAGGAACGACCGATTTCCAGGC
CTAAATCAAAATTTCAGATGCAAGAAAGACCAGACACATTGGCGGCAAGCT
AATGAGAAGCTAGATAAGTGAGTCACTCGGCAACTTTCTGCTACTTTTACCT

8th exon (nucleotides 25765 to 25861)
GCTTTAATTTGACCTCTTGTTGTTTCCTAGAACAAAGGCCGAGTTAGATCAAG
AAGCCTTGATCAGTGGCAAACTCTGGCTACAGAAGCACATTTAATCATCCTGGA
TATGCAGGAAAACATTATCCAGGTGAGGAAAACAAACACCCAATCTGATTTG

9th exon (nucleotides 27242 to 27376)
GGATTCAATGATGCTGTTCTTCCATTCCCCCAGGCGAGCTCGGCTCTGGACTG
TAAAGACAGCCTGCTGGAGGTGTTCTGAGGTGCTGGTGAATTCTCTGAAC
TGTGATCAGATGACCACCTACCTGACTCACTGCTTTGCAACACTCCGTGCTCT
CATCGCCAAGGTAAATTTGGGATGCTTGTTTTCTTCCTCTTAATT

10th exon (nucleotides 28582 to 28734)
AGTGATGCCTAATGGCCCTTTATGTCTCTCCTAGTTTGGAGACTTACTCTTCG
AAGAGGAGGTGGAACAGTGTTTCGACCTATGTCACCAAGTCCTGCACCACTG
CAGCAGCAGCATGGATGTCACCCGGAGCCAAGCCTGTGCCACCCTTTACCTC
CTCATGAGGTTCAGTTTTGGAGCCACCAGTGTAAGAGTTCAAACCAGCTGAG
TGACCTGGAATCAG

11th exon (nucleotides 31046 to 31204)
TTACTTCATCTTTTTTTTTTTTTTCACTGATGCAGAATTTTGCAAGAGTAAAGA
TGCAAGTAACCATGTCCCTGGCATCTTTGGTGGGAAGAGCACCAGACTTTAA
TGAAGAGCACCTGAGAAGATCCTTGAGGACAATTTTGGCCTATTCAGAAGAG
GACACAGCCATGCAGATGACTCCTTTTCCCACCCAGGTACACCGAAGCACAT
ACCTTGTCTCATGCATGAGT

12th exon (nucleotides 32755 to 32853)
AGTTAAGATTATTTTAAGCTTACACTTTTTGCAGGTGGAGGAACTTCTCTGT
AATCTGAATAGCATCTTATATCACACAGTTAAAATGAGGGAATTTCAGGAAG
ATCCTGAGATGCTTATGGATCTCATGTACAGGTAAGCTTTCCTGACACACTCA
AGGGACACCATTT

13th exon (nucleotides 33663 to 33855)
TCCTCAAAACTATTCTCACTCAATCTGTCTTCAGAATTGCCAAGAGTTACCA

FIG. 7A (2 of 4)

14th exon (nucleotides 38125 to 38268)
CTGTTCTCCAGGCTTATACTGTGGTCTCTTTCAGAATATTTCTTCCAATGTGCT
GGAGGAGTCTGTGGTCTCTCAGGACACCCTGTCACCTGACGAGGATGGGGTGTG
CGCAGCCCAGTACTTCACCGAGAGTGGCCTGGTAGGCCTCCTGGAGCAGG
CCGCGGAGCTCTTCAGCACGGTCAGTGCCCAGAGGGCATCCCGGGGCCTGGC
C

15th exon (nucleotides 40166 to 40297)
AATTCTCTCTGATGCTCTTCTCCTCTTCCAAGGGAGGCTTATATGAGACAGT
TAATGAGGTCTACAAGCTGGTCATCGCCATCCTAGAAGCGCATCGAGAATTC
CGGAAGCTGACACTCACTCACAGCAAGCTGCAGAGAGCCTTCGACAGCATCG
TTAACAAGGTAGCCGGGGAGCTCTGGCTGGCAGGTCTTGTTAC

16th exon (nucleotides 40755 to 40889)
TAAGGAGAGCTTTTTATATTTTGTTCCTCAGGATCATAAGAGAATGTTTGGAA
GCTACTTCCGAGTTGGTTTCTTTGGATCCAAATTTGGGGATTTGGATGAACAG
GAGTTTGTCTACAAAGAGCCTGCAATTACCAAGCTTCCTGAGATCTCACATAG
ACTAGAGGTAAGAAAAGTGATTCTGTGCGCCTGACCTGGTACACTTTAC

17th exon (nucleotides 42307 to 42396)
AACCTTTATAAACTGTTGGTTCTTCTTACCTAGGCATTTTATGGTCAATGTTTT
GGTGCAGAATTTGTGGAAGTGATTAAAGACTCCACTCCTGTGGACAAAACCA
AGTTGGATCCTAACAAGGTATACAAAAATTTACAAAAACTAACCATCAAGC

18th exon (nucleotides 45250 to 45486)
TCTTCTCCCTCCTGTGCCTTTTCCCGCTTAGGCCTACATACAGATCACTTTTGTG
GAGCCCTACTTTGATGAGTATGAGATGAAAGACAGGGTCACATACTTTGAGAAGA
ATTTCAACCTCCGGAGGCTCATGTACACCACCCCGTTCACCCTGGAGGG
GCGGCCTCGGGGAGAGCTGCATGAGCAGTACAGAAGGAACACAGTCCTGAC
CACTATGTACGGCTTCCCCTACATCAAGACTAGGATCAGCGTCATCCAGAAG
GAGGAGCTAATCCACCAAGTGATTGGCACCATTGATGAGT

19th exon (nucleotides 45664 to 45807)
ACAGTGACTTCCCTATGTTTACGTCTCATGTTCAGTTTGTTTTGACACCGATTG
AAGTTGCCATTGAAGACATGAAGAAGAAGACCCTGCAGTTAGCAGTTGCCAT
TAACAGGAGCCGCCTGATGCAAAGATGCTTCAGATGGTGCTGCAAGGCTCTGT
GGGAGCTACTGTAAATCAGGTAAGCAAAACCAGAGGTGGCAGCTCCT

[illegible]

FIG. 7A (3 of 4)

21st exon (nucleotides 62398 to 62568)

TCATTTATTTCTCCCACACTGATATTTTCATCTCAGATGTGGTGAAGCTGTAG
AGAAAAACAAGCGTCTCATCACGGCAGACCAGAGGGAATATCAGCAGGAAC
TCAAAAAGAACTATAACAAGCTAAAAGAGAACCTCAGGCCAATGATCGAGC
GGAAAATTCCAGAACTGTACAAGCCAATATTCAGAGTTGAGAGTCAAAAGAG
GTAAGAACAGGGCAGAGGAGGCCTCTTCCTGTGGGAT

22nd exon (nucleotides 63040 to 63294)

GCTCCCTCTCTTTTCTTAATTTCAGGGACTCCTTCCACAGATCTAGTTTCAGGA
AATGTGAAACCCAGTTGTCACAGGGCAGCTAAGAAAAGCCATCTTCATTCGT
GGAGACTGTGGCCCTGCAACCCTGGAGAAGGACTTGCTGGTACTTAAAAAAT
GGGACATTTGCCACCCAGGACTGACTGTACACTCCCTGATCAGCCAGCACTC
TGGAAGCTTTGGGATCCCAGGAACCATGGAATTATTCCCAAATGGACTCTGA
CCAGATTTTTGCCATACTGGGGGGTGGCGGGATGGAGGATGGGTACTCAGGC
ATGACTGCGTATTCATTAAAGTGTGTTTTTCCACAATGTACCAAACAAGGCAT
AAGCAGCTTCTCCTGCTGACTGGCCAATCACTGCCCATCTGAGAGATGATTTC
CTCTGGCCCATATTTGAATTTATTGGAGTAACTCAAATTGCCTGAGGAAAAAT
GGAAAAATTATCCACCAGTCGATTCAAACTGAATTTCACTCTTTATAGGAAG
GCAGGGCAAACTTGTAGGAGTACGAAACATTTTCAATAAATCTACAAAGGGA
AGCCTTACTACAATTCCAAAAATCATCATGGTTGGAAATTTGGGAGGAGATT
ATTTGTGAACTTGTTACCCTTTTGGTAATGGTGGACTAATTGCTGTATAGTTAT
TTTTGTTTTATTATTACTGTTACATTAATTTAACATGCATTTATAGAAGAATAC
ATTCAAAGCACTGATGTAGGAGATACACGGTACTTGGAGCAGTCAGCCAAAA
ATCACAGATACTGCTTTCACTTAAATGGAAACAATTCTCCGATAATGCTTTGC
TTTTTTTCTTATGTCACTCTTGTGTACTATCTATTTTTCTCCTCTCTGGGACCAA
GTTTCTTTTTATAAAGCAATAATATCTCTGTTTTCATTTCAGAACATTGTGCTG
TCTGTCAGCATATGTATATCAGCTACAAAATATATTCAACTTTGACTTCTTTTG
ACAAAGGACTTTAGGAAAAGGAGGAACAAAGACATTATTTGAGAATTAAATT
ATATATTTTTAATATGACTGTGACCTTGACTGATAATAAAGATGTAATAAGAA
TTGCAAGCTAAAAAAAAAAAAAAAAAA

FIG. 7A (4 of 4)

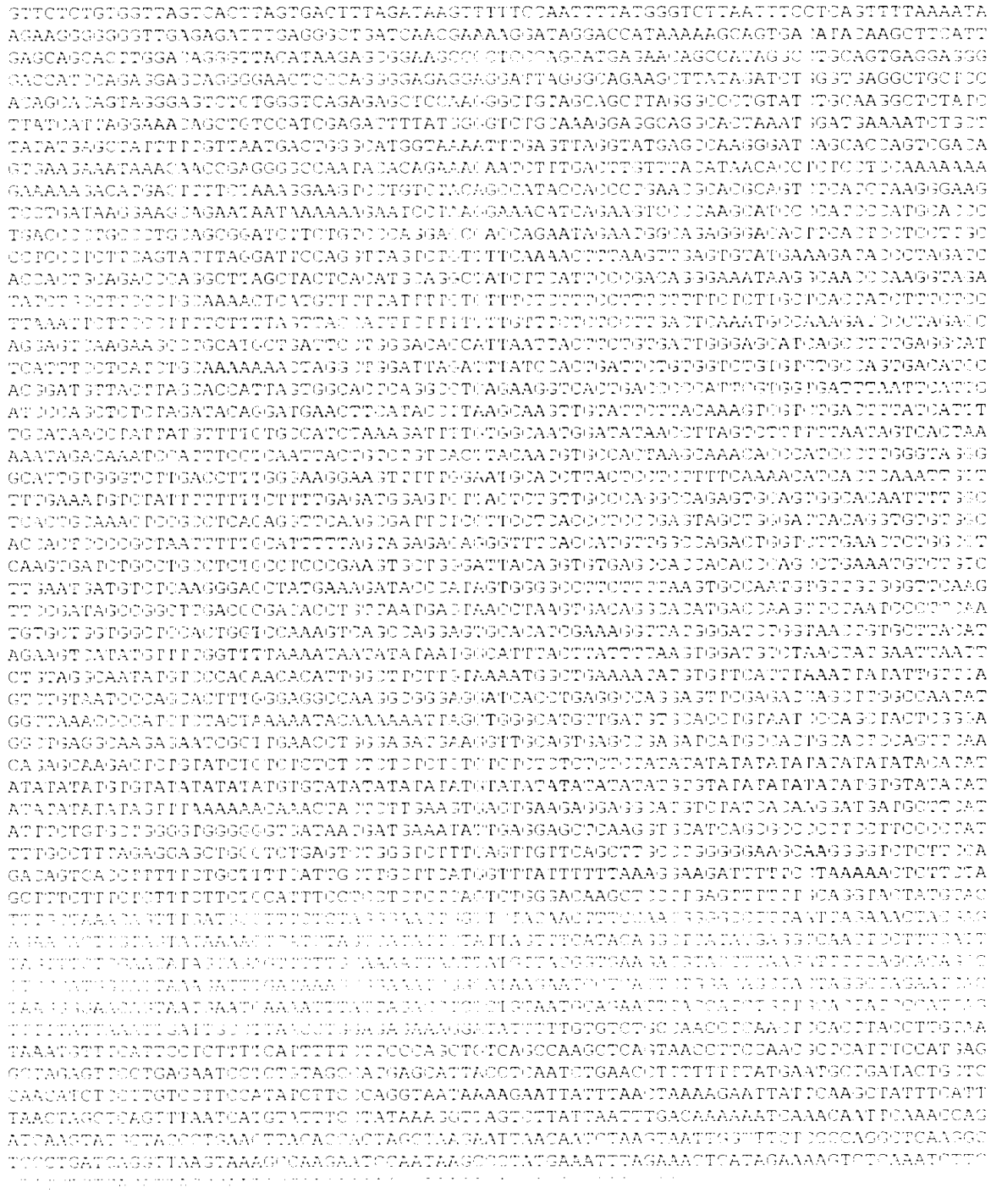


FIG. 7B (1 of 15)

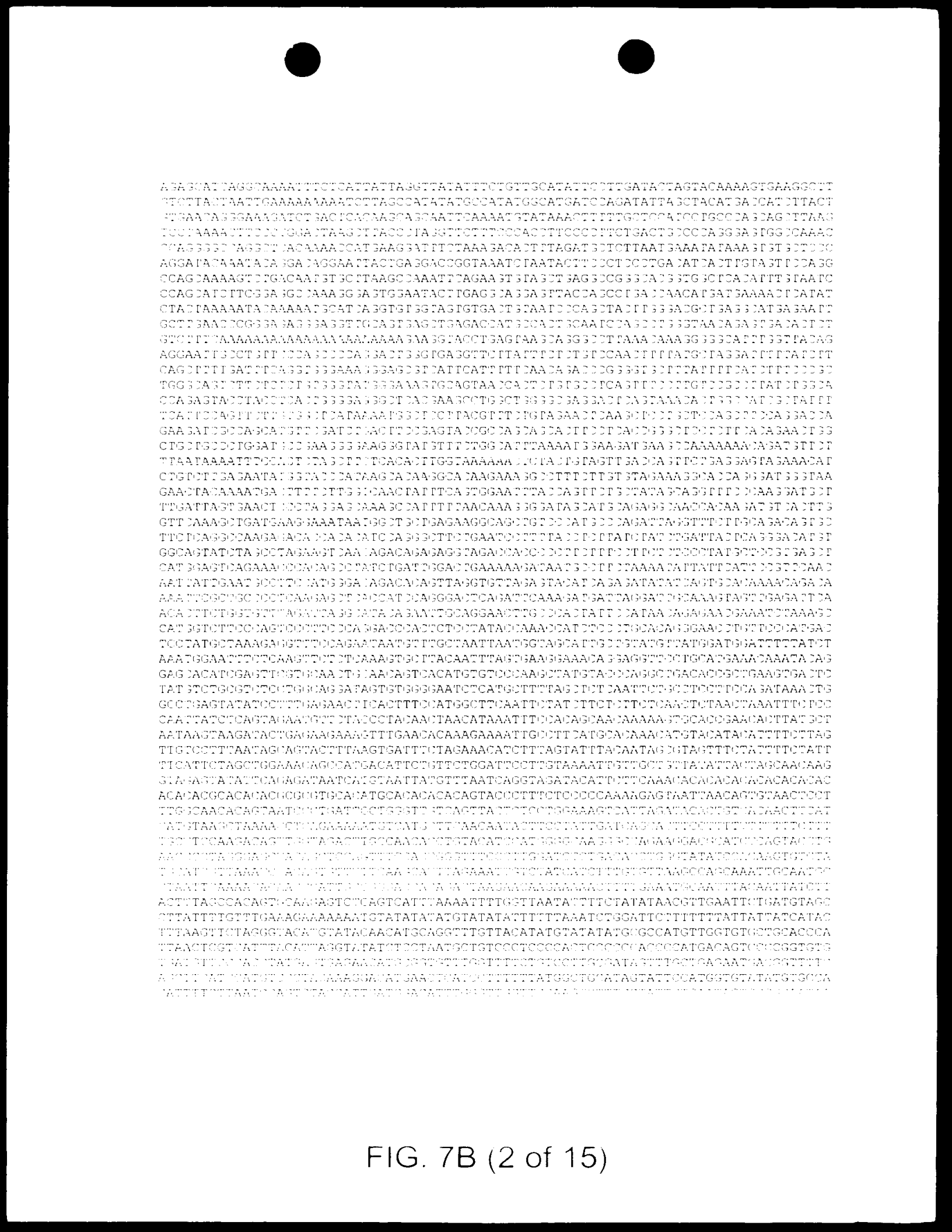


FIG. 7B (2 of 15)

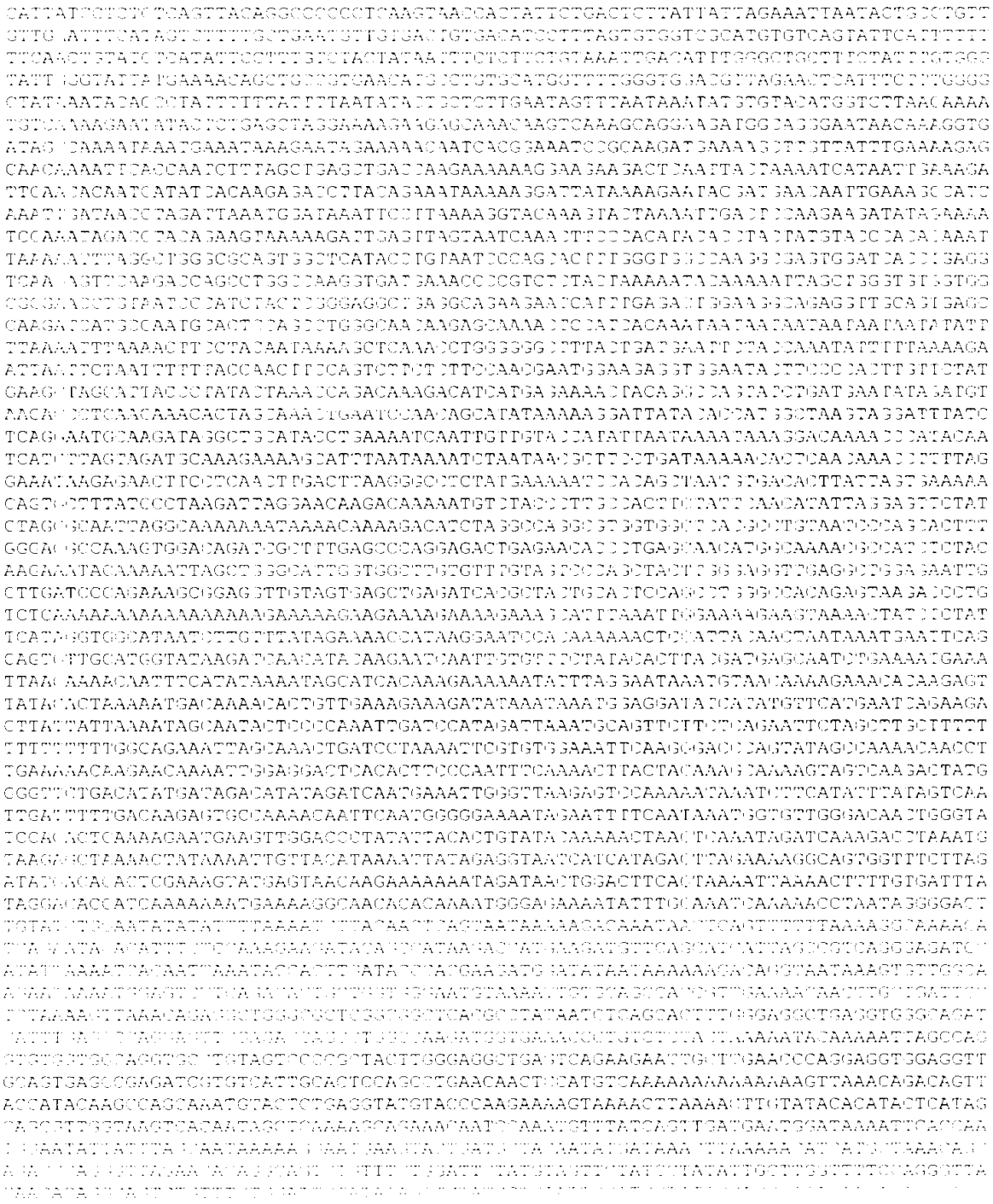


FIG. 7B (3 of 15)

FIG. 7B (4 of 15)

FIG. 7B (5 of 15)

FIG. 7B (6 of 15)

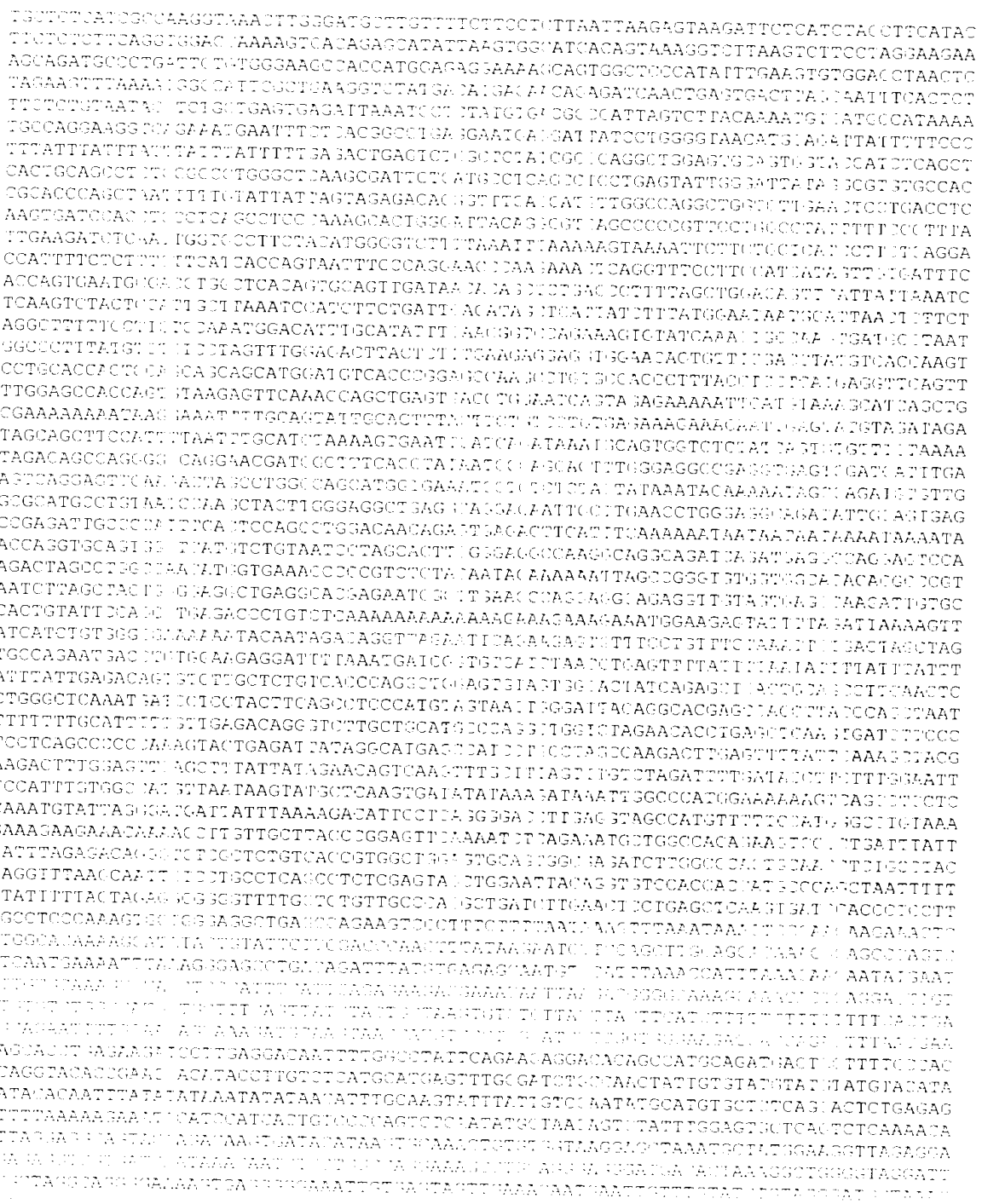


FIG. 7B (7 of 15)

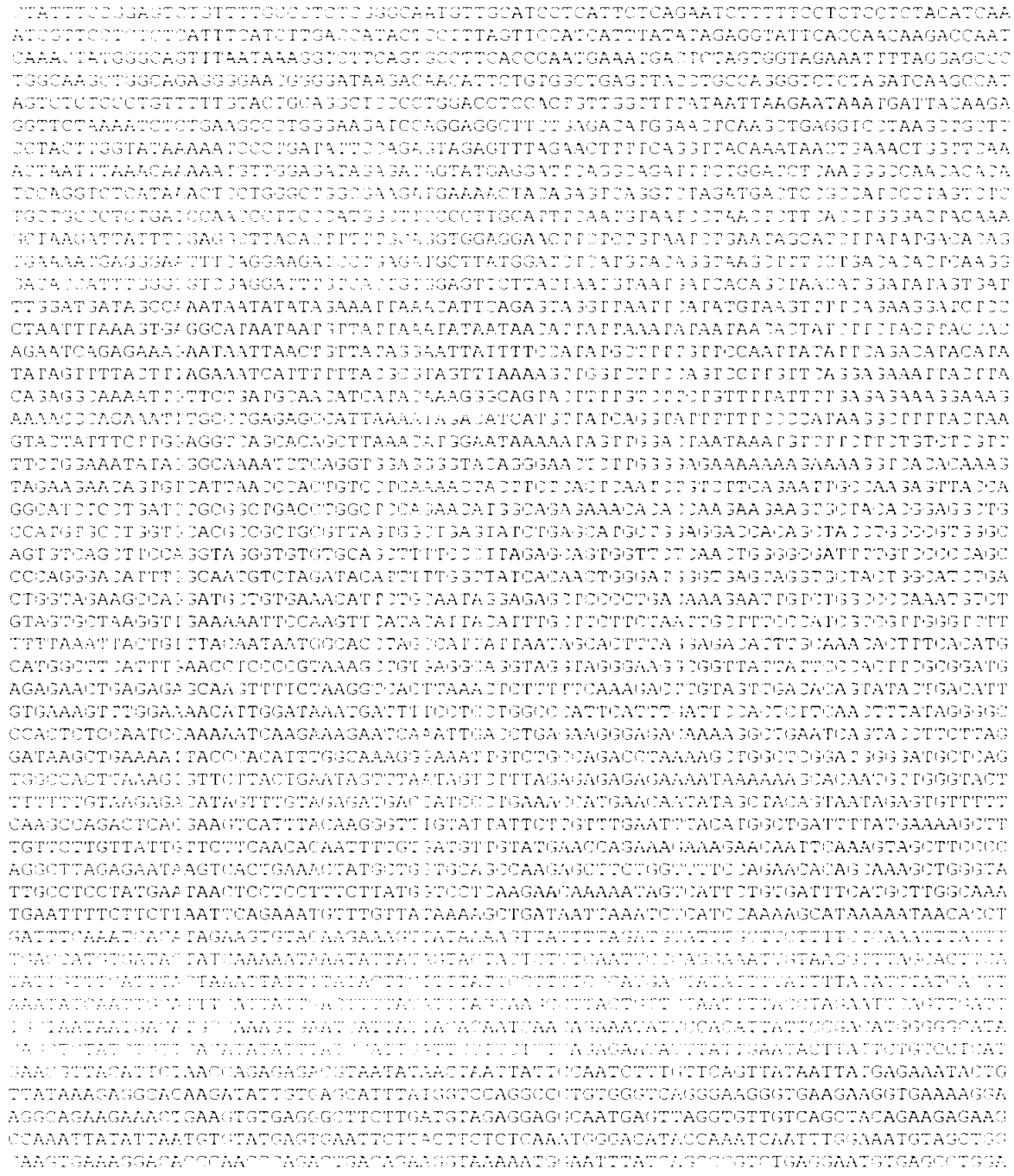


FIG. 7B (8 of 15)

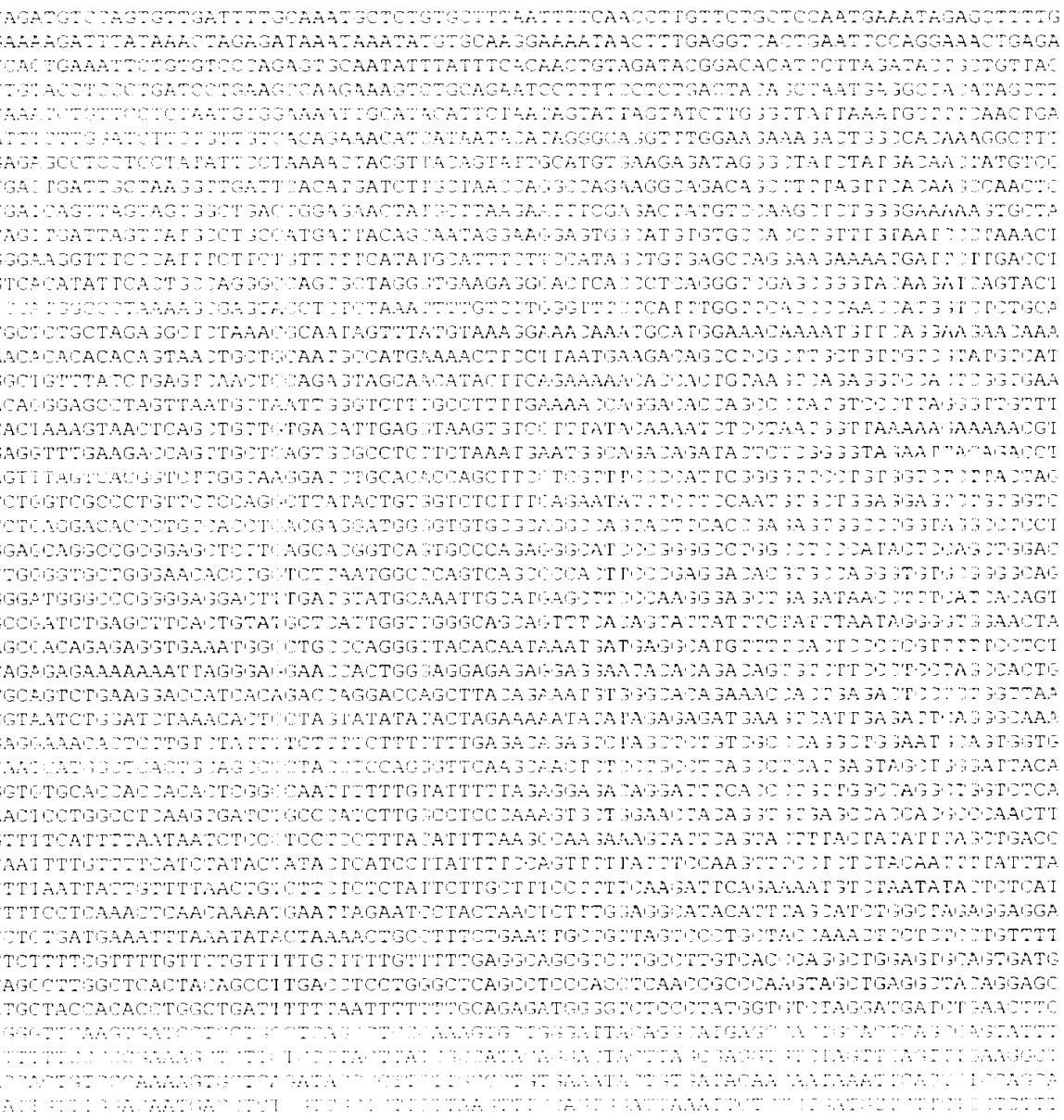


FIG. 7B (9 of 15)

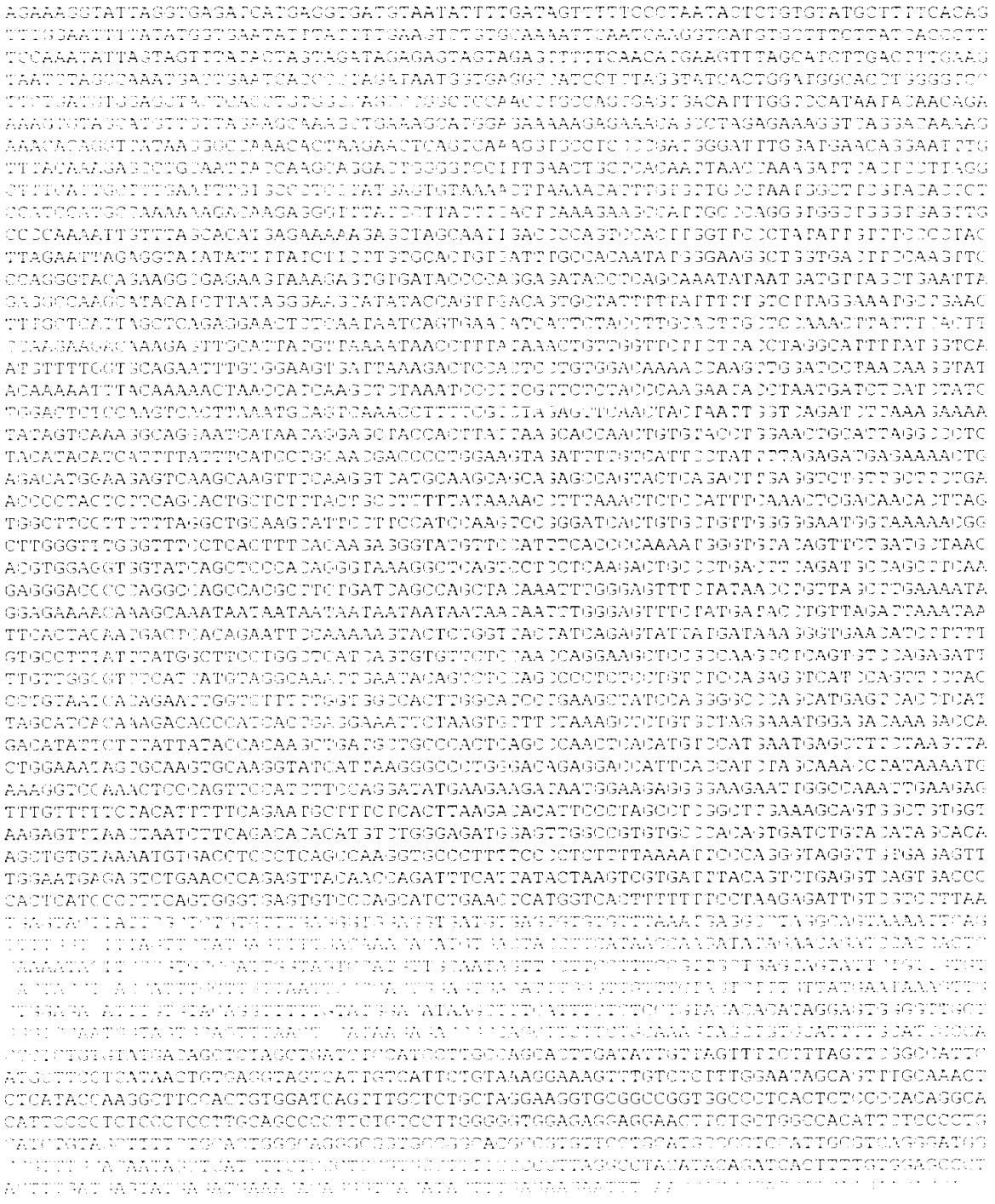


FIG. 7B (10 of 15)

FIG. 7B (11 of 15)

FIG. 7B (12 of 15)

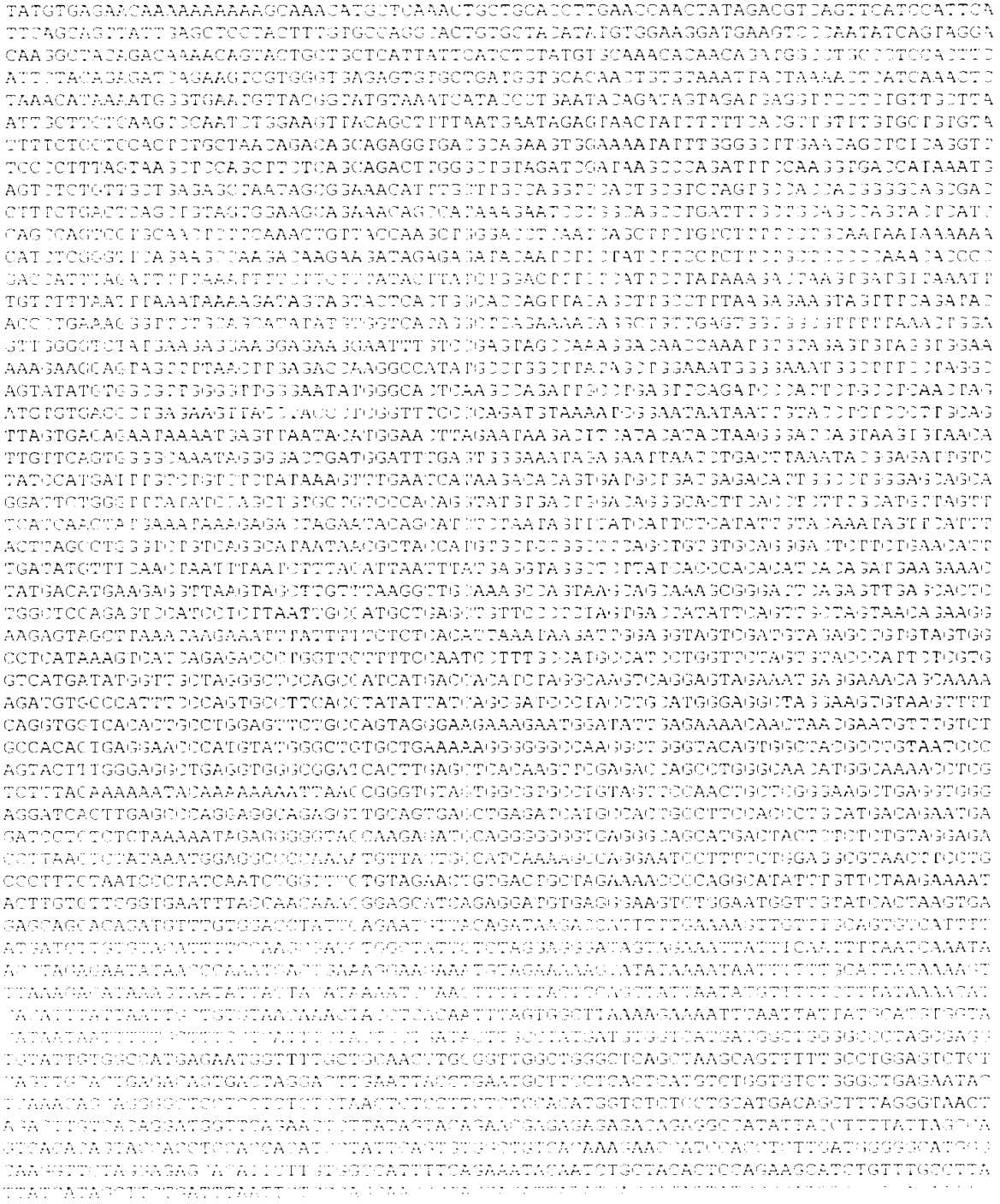


FIG. 7B (13 of 15)

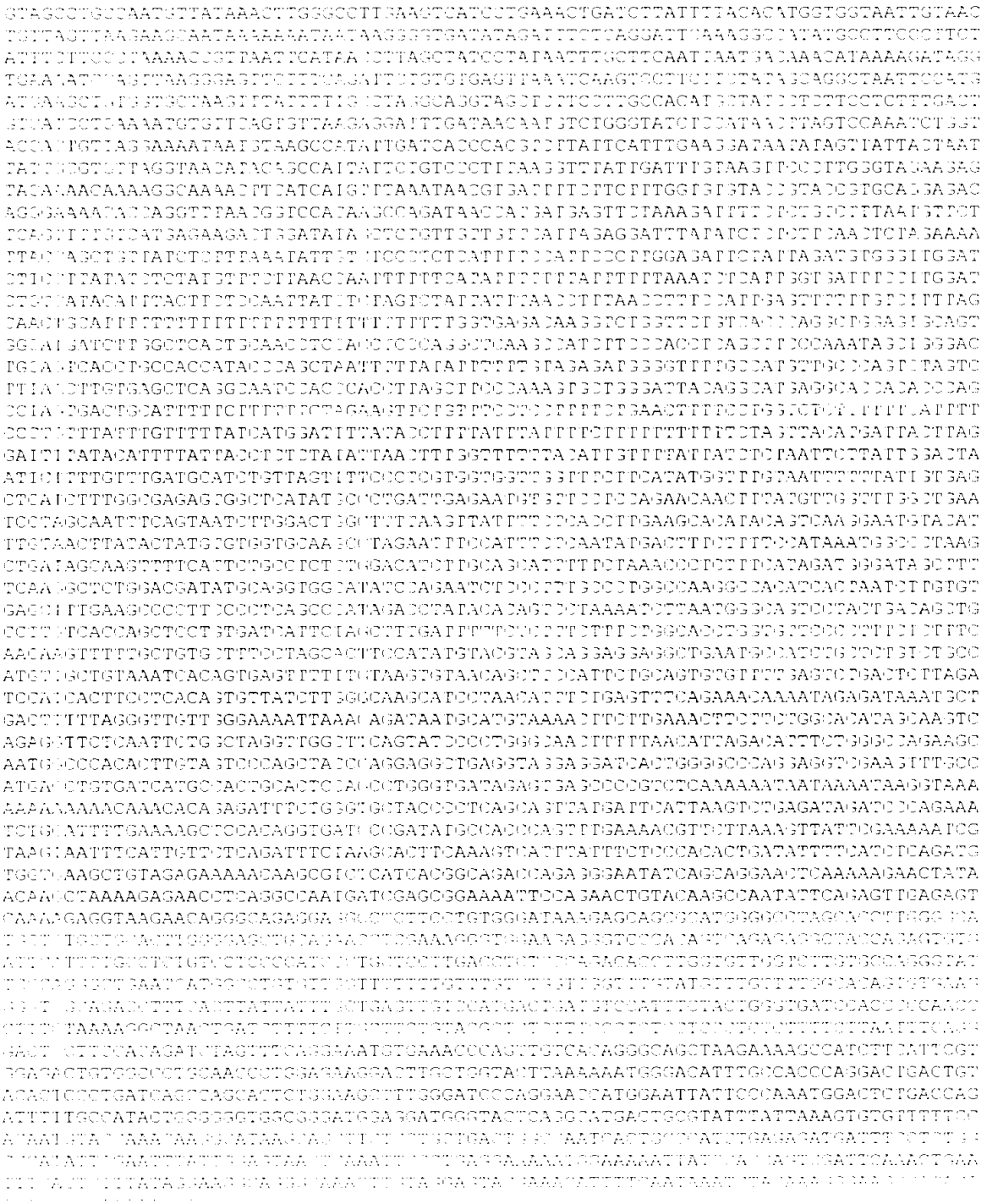


FIG. 7B (14 of 15)

FIG. 7B (15 of 15)

GGAACAATTTCCTCTCATGTGTATGGCTGCCTAAAGTGTTGGCTGAGCATTGTCCACATGGGTG
ATGTAAAGGATCACTGAACTAGGAGCAGTTGGGAAAAAATACAATCATTGGGAATTCCTGTAGC
ATGTAATGTGCTTACAGGGAGGTAAAAGTATTCATACAACAGTTCTCTGGTGTTCTCTGTTGTA
GCAACCAGTCAGCCAAAAGGGTTCATGTGCTTGAAATGAGAATGGCTGGATCAAAATGGCAGCT
CATGATTTAAAGGATTCTAGTCAGATACCAGACATCCTCACATAGAGAAAACTCTGAATGGCTG
GGGGAGAAGGAGTCAAATGCCCTGGATCTTTTTCTTGGGCCTCAAAGTCCTCCTTCTGTCATCA
TCCTTCCAGTATTGGCAGGACCTGACTGCAGGCATCATGGCCTCTGTGAACTTCTCAAGGGTA
TGTATTATCTGACAAAAACTACGATGTCCACTAACAGGCCACTGAAAGGTATCTTAGTCAGTTC
TGGTCATTGCCCAGTCAAGGCCTACGTTTTATAACATGATATCAAAGATTGCATCTAAAATTGT
GATGATTTCCTAAAATAATCATTTCATTTAGATTTTTCTATTTTAATCCAAGGTATTCTTCCAGC
AGAAATAAGGAAACAGTTTACTCTCTCCACCAAACCTTGGCCAGTACCATCGACAGAGCATAAGT
ACCTCTGGCTTCCCCTCTCTTCAACTAGTAAGTATGAGTTCCAGGTTTACTTAGCGATTGGTCA
AGTGCAAAAGTGCCCAGGGTATGTGTTTGCCTCCTGTTCCTTAGATCTTCCTACCATCACCTCA
CATTCTCCAGTCACCAGATCCTAACTCTGTGACTGTGTCTCGGACATCAGACAATATCCCCTCT
CTCTCTGCCAACCGGTACTTATGGTACATAATAGAACCTCTGGGAGCTGTGTGGTTTTGATGTCTC
TAGACTAGGTGGGCTTCCAGCTGACTCAGTCTCATCCAAATTATGGTTCATATTTGGGGGAGAA
GGGCTAGCCCAAAAACTTACCACCATTTGTAGTATGCATTTTTTTTGGAAAAGCATATTCCAAAA
TCTGAAATGCCAAGTTAGAGACCTCCTTTTTGTAAAATAATTTTCTTGCTAGTATAATTTACAT
ATAATAAAATTCACACATTTTAGGTGTACAATTTGGTGAACTTGGGCAACTTAGAGTCACTTAA
CCTTTCCTCAGTCAAGATATAGAACACTTCTTTTATCCTAAAGCGTTCCCCAGCGCGCTTTTAC
AATGTCCTCTCCCCAGGCCACACCCTCCAACTCACGCAATCTCTGACTCACTTCTGTCACCATA
ATTTTGCTCTATCTGGAGCTTCATATCCTGTTACAGTATGTACAAACCTTCTTTTTTTGAGACA
GGGTGTCAGTCTGTCACCCAGCCTGGAGTACAGAGGTGTGATCTCAGCTCACTGCAACCTCCAAC
CTCCCAGGATCAGATGATTCTCCTCCCACCTCATCCTCCCAAGTAGCGGGACTACAGGCGCAT
GCCACCACACCTGGCTAATTTTTGTACTTTTTGTAGAGACAGGGGTCTTGCTATGTTGCCCAGG
CTGGTCTTGAACTCCTGGGCTCAAGCGATCCTCCTGCCTCAGCCTCCCAAAGTGCTGGGATTAC
AGTGAGCCACTGCACCTGGCCCTAAACCTTCATTTTTAAAACACATTTCCTCTTAAATTGAAGA
TTGCCTACATTTTTATATCAATGCCAATTGTTGAGTGTGCCTATATGTGTTATATTATTGAGC
ACTAAATGCCAGATGTGTGCCAAGTGAGATAAATCTGACAAATGAGATGGTTTGTAAAACCAGC
AGTGAATATTCACTTCCTCTGTGAGAGAGCTCCAGCCCTCCTGTACTCACTTCCTCACACAGCA
CAGCAGCACTCTTGCTGGTTCTGCTGCTTATCTTGAAGAGGTTAGGTTACTTTTTGTTTCTACT
TATTACTTCGAAACCACTTCTGCCTTAGAAATTTTGTAACCTTCCGCTCAGTTTCCGGTAACCG
CCATTTTGTCTCCTGTAACAATTTACGCGCCGTGTAACTGTGAATCTTT

FIG. 7C

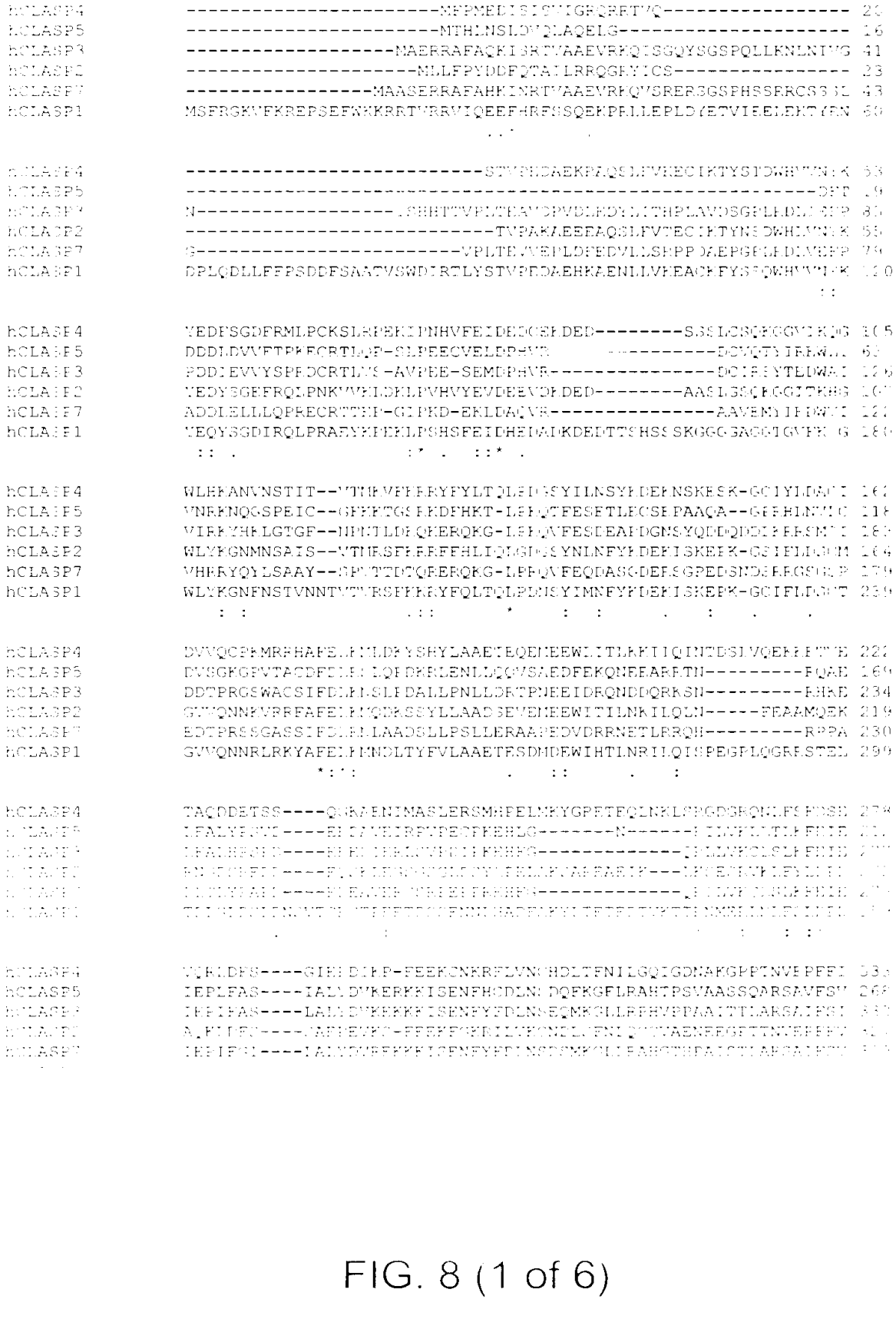


FIG. 8 (1 of 6)

FIG. 8 (2 of 6)

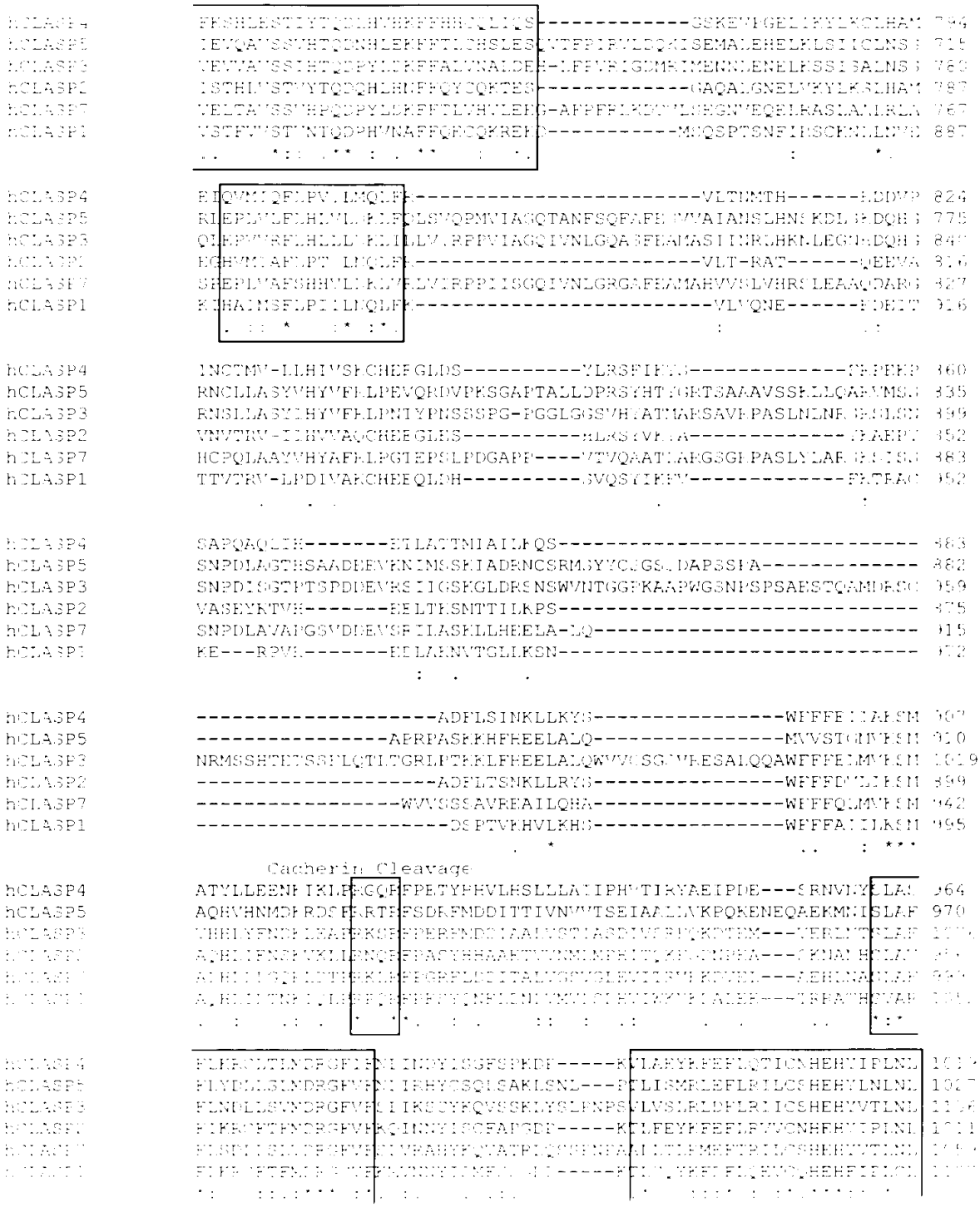


FIG. 8 (3 of 6)

FIG. 8 (4 of 6)

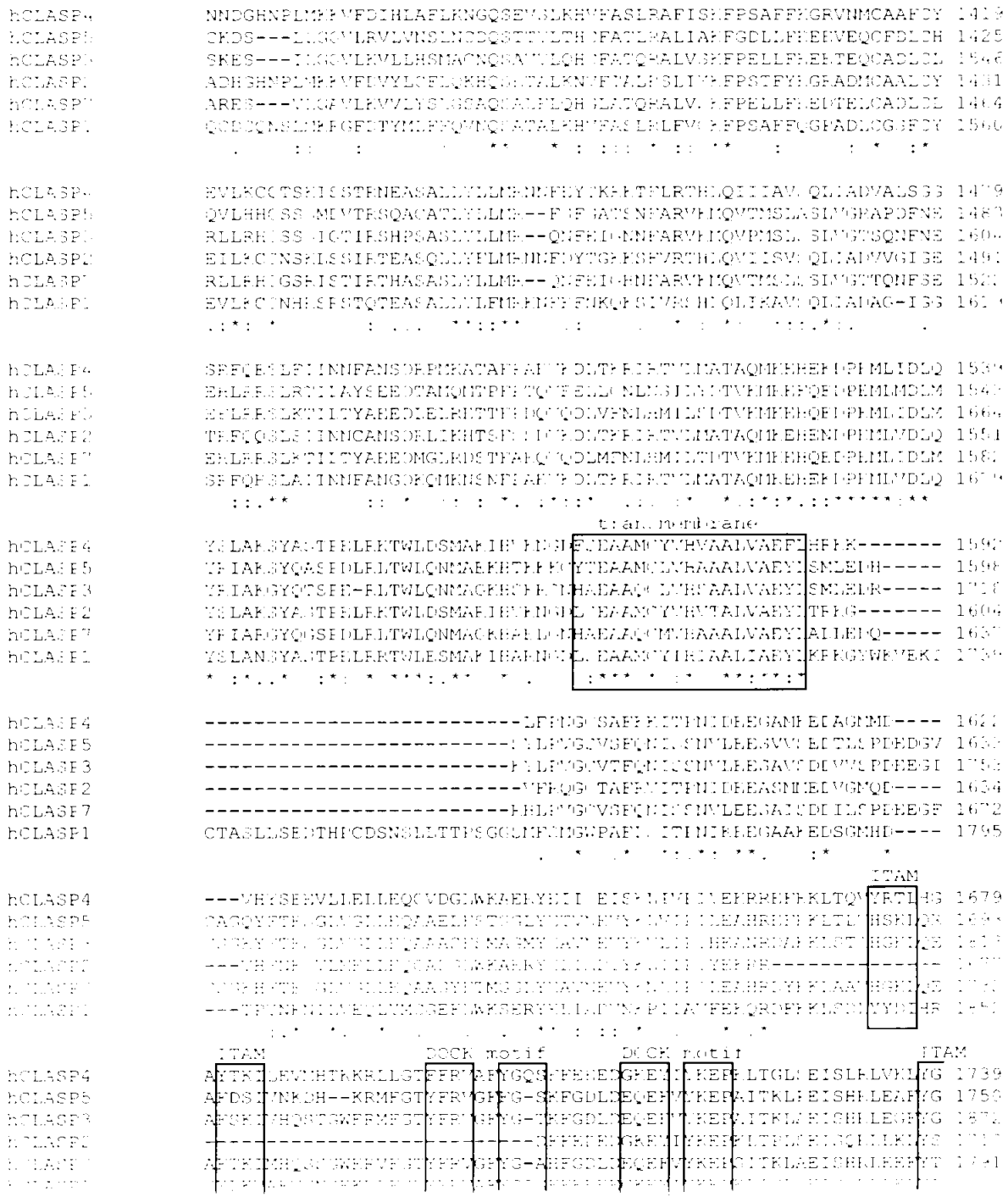


FIG. 8 (5 of 6)


ITAM
ITAM
ITAM
DCCE motif
Coiled-coil
Coiled-coil
PEST ligand
hCLASP4
hCLASP5
hCLASP3
hCLASP2
hCLASP7
hCLASP1

FIG. 8 (6 of 6)